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<p>(54) Title: CLONED PORPHYROMONAS GINGIVALIS GENES AND PROBES FOR THE DETECTION OF PERIODONTAL DISEASE (57) Abstract <p>DNA fragments from <i>Porphyromonas gingivalis</i> which express <u>hemagglutinin</u>/proteases that elicit anti-<i>P. gingivalis</i> immunologic responses are described. Microorganisms, genetically modified to express <i>P. gingivalis</i> antigens, are provided. Also disclosed are probes, vaccines, and monoclonal antibodies for the detection and prevention of periodontal disease.</p><p><i>cf. 6, 11 (serials No. 8)</i></p></p>		

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DESCRIPTIONCLONED PORPHYROMONAS GINGIVALIS GENES
AND PROBES FOR THE DETECTION OF PERIODONTAL DISEASE

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The subject invention was made with government support under a research project supported by the National Institutes of Health Grant Nos. DE 07496 and DE 00336. The government has certain rights in this invention.

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Cross-Reference to a Related Application

This is a continuation-in-part of co-pending application Serial No. 08/353,485, filed December 9, 1994, which is a continuation-in-part of application Serial No. 07/647,119, filed January 25, 1991; which is a continuation-in-part of application Serial No. 07/241,640, filed September 8, 1988, now abandoned.

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Background of the Invention

Periodontal disease (PD) is a chronic inflammatory disease which results in the destruction of the supporting tissues of teeth. Although the specific microbial etiology of PD is not known, it is widely accepted that bacteria are the contributing agents of the disease.

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The presence of a complex microflora in the subgingival crevice has complicated the identification of the specific etiologic agents of PD. However, it appears that a few genera, primarily gram-negative anaerobes, are associated with disease progression. Several lines of evidence strongly implicate the gram-negative anaerobic bacterium *Porphyromonas gingivalis*, previously known to those skilled in the art as *Bacteroides gingivalis*, as an etiological agent of adult periodontal disease (White, D., D. Mayrand [1981] "Association of Oral *Bacteroides* with Gingivitis and Adult Periodontitis," *J. Periodont. Res.* 1:1-18; Takazoe, L., T. Nakamura, K. Okuda [1984] "Colonization of the Subgingival Area by *Bacteroides gingivalis*," *J. Dent. Res.* 63:422-426. For example, relatively high proportions of *P. gingivalis* have been isolated from adult periodontitis lesions, patients with adult periodontitis have been found to have higher levels of IgG antibodies to *P. gingivalis* than do normal adults, and local immunity to *P. gingivalis* is greater in the more advanced cases than in the early forms of periodontal disease. *P. gingivalis* also appears to be a causative agent of experimental periodontitis in animals (Slots, J., E. Hausmann [1979] "Longitudinal Study of Experimentally Induced Periodontal Disease in *Macaca arctoides*: Relationship Between Microflora and Alveolar Bone Loss," *Infect. Immun.* 23:260-269). In

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addition, *P. gingivalis* possesses a variety of suspected virulence factors such as proteases, collagenases, immunoglobulin degrading enzymes, and adhesins.

In order to exert their pathogenic effects, periodontopathic bacteria such as *P. gingivalis* must possess characteristics which enable them to colonize the host, survive in the periodontal pocket, possibly invade the gingival tissues, and to destroy the collagenous periodontal ligament, the alveolar bone, and other tissue components surrounding the tooth. Components of bacteria which mediate attachment to host tissues include surface structures such as fimbriae, capsular materials, lipopolysaccharides, and membrane-associated extracellular vesicles.

The hemagglutinating activity of *P. gingivalis* has been studied as a parameter that affects the adherence of this organism in the periodontal pocket. Sera from patients with adult periodontitis possess high antibody levels to the *P. gingivalis* hemagglutinin. It is thus suggested that the adhesive surface structures such as hemagglutinin participate in *P. gingivalis* colonization and antigenic stimulation of the host.

Investigations have reported the isolation of hemagglutinin activity from *P. gingivalis*. Boyd and McBride (Boyd, J., B.C. McBride [1984] "Fractionation of Hemagglutinating and Bacterial Binding Adhesins of *Bacteroides gingivalis*," *Infect. Immun.* 45:403-409) prepared an outer membrane component containing hemagglutinating activity from *P. gingivalis* W12. This preparation contained three major proteins with molecular weights of 69,000, 41,500, and 22,000. Inoshita *et al.* (Inoshita, E., A. Amano, T. Hanioka, H. Tamagawa, S. Shizukushi, A. Tsunemitsu [1986] "Isolation and Some Properties of Exohemagglutinin from the Culture Medium of *Bacteroides gingivalis* 381," *Infect. Immun.* 52:421-427) isolated hemagglutinating activity from culture supernatants of *P. gingivalis* 381. The isolated hemagglutinin component contains three major proteins with molecular weights of 24,000, 37,000, and 44,000. Okuda *et al.* (Okuda, K., A. Yamanoto, Y. Naito, I. Takazoe, J. Slots, R.J. Genco [1986] "Purification and Properties of Hemagglutinin from Culture Supernatant of *Bacteroides gingivalis*," *Infect. Immun.* 55:659-665) also purified a hemagglutinin of *P. gingivalis* 381 from culture supernatant which appears to have vesicle or tubelike structures and is comprised mainly of a 40,000 molecular-weight protein. Their recent report indicated that sera from most patients with adult periodontitis reacts to the hemagglutinin antigen at 43,000 and 57,000 molecular weights (Naito, Y., K. Okuda, I. Takazoe [1987] "Detection of Specific Antibody in Adult Human Periodontitis Sera to Surface Antigens of *Bacteroides gingivalis*," *Infect. Immun.* 55(3):832-834).

Recombinant DNA techniques have proven to be powerful tools for the study of pathogenesis. However, recombinant DNA techniques have been applied only sparingly to the study of gram-negative anaerobic pathogens and even less to the study of the molecular mechanisms of

periodontopathogenesis. The recombinant DNA methodologies offer advantages over previous methods used in the study of oral pathogens. For example, the cloning of *P. gingivalis* antigens allows for a genetic and molecular analysis of the gene(s) which presently is difficult due to the lack of knowledge about the genetic system in *P. gingivalis*.

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Brief Summary of the Invention

Genes have been cloned and the proteins encoded thereby have been isolated from organisms associated with periodontal disease (PD). In particular, genes from *Porphyromonas gingivalis*, which is an etiological agent of adult PD have been identified, characterized, and sequenced. These genes have also been ligated to an appropriate vector and used to transform an appropriate host cell. The recombinant cells express antigens which elicit immunological responses. Antigens expressed by the *P. gingivalis* clones are also identified and described here.

The invention provides, *inter alia*, a means of detecting the presence of disease-causing *P. gingivalis*. The detection method involves the use of DNA probes and antibody probes which selectively identify the presence of these bacteria or can be used to identify other organisms, including other prokaryotes or eukaryotes, which have similar nucleic acid or amino acid sequences. Also provided are polypeptides which can be used for the production of antibodies to the organisms associated with PD. The antibodies selectively and specifically bind to the subject proteins and can be utilized in purification and identification procedures. These genes and polypeptides can be used as a vaccine against PD. Further, a means of producing monoclonal antibodies for the antigens associated with periodontal disease is also provided.

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Brief Description of the Drawings

Figure 1 shows a schematic diagram of restriction enzyme recognition sites of recombinant plasmids from clones 2, 5, and 7. The solid lines represent *P. gingivalis* DNA inserts. The hatched boxes represent pUC9 regions.

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Figure 2 shows a restriction map of a hemagglutinin gene, *hagB*. The hemagglutinin gene is contained on a *HindIII* fragment in pUC9.

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Figure 3 shows a restriction enzyme map of cloned *EcoRV* fragments of *P. gingivalis* 381. The heavy shaded area designates the originally cloned ST2 fragment; the thin shaded area designates the amplified IPCR fragment.

Figure 4 shows the restriction enzyme map of the *prtP* gene. The top line represents the *prtP* gene sequence; the bottom line represents the gene product. Restriction sites shown are: B, *BamHI*; N, *NspI*; A, *AspEI*; S, *SacI*; X, *XcmI*. Fragments used as probes for Southern blot analyses

are shown as heavy bars below the DNA sequence and in the comparable position below the protein sequence. The DNA region homologous to IS1126 is underlined. Regions repeated within the protein are shown as identical boxes, and the Pro-Asn repeat region is indicated by an asterisk. Putative autodegradation cleavage sites and the signal peptide cleavage site are indicated below the gene product.

Brief Description of the Sequences

SEQ ID NO. 1 is the nucleotide sequence of the hemagglutinin gene designated *hagA*.

10 SEQ ID NO. 2 is the derived amino acid sequence of the polypeptide encoded by the *hagA* gene.

SEQ ID NO. 3 is the nucleotide sequence of the hemagglutinin gene designated *hagB*.

SEQ ID NO. 4 is the derived amino acid sequence of the polypeptide encoded by the *hagB* gene.

SEQ ID NO. 5 is the nucleotide sequence of the hemagglutinin gene designated *hagC*.

15 SEQ ID NO. 6 is the derived amino acid sequence of the polypeptide encoded by the *hagC* gene.

SEQ ID NO. 7 is the nucleotide sequence of the hemagglutinin gene designated *hagD*.

SEQ ID NO. 8 is the derived amino acid sequence of the polypeptide encoded by the *hagD* gene.

20 SEQ ID NO. 9 is the nucleotide sequence of the gene designated *prtP*.

SEQ ID NO. 10 is the derived amino acid sequence of the polypeptide encoded by the *prtP* gene.

SEQ ID NO. 11 is primer APF 147 used according to the subject invention.

SEQ ID NO. 12 is primer APF 148 used according to the subject invention.

25 SEQ ID NO. 13 is the nucleotide sequence for the entire *hagA* gene obtained from the *EcoRV* fragment of the *P. gingivalis* strain, according to the subject invention.

SEQ ID NO. 14 is the deduced amino acid sequence of the polypeptide encoded by the entire *hagA* gene.

30 SEQ ID NO. 15 is the nucleotide sequence of the first approximately 1.3 kb repeat sequence from *hagA*, designated *HArep1*.

SEQ ID NO. 16 is the deduced amino acid sequence of the polypeptide encoded by *HArep1*.

SEQ ID NO. 17 is the nucleotide sequence of the second approximately 1.3 kb repeat sequence from *hagA*, designated *HArep2*.

SEQ ID NO. 18 is the deduced amino acid sequence of the polypeptide encoded by *HArep2*.

SEQ ID NO. 19 is the nucleotide sequence of the third approximately 1.3 kb repeat sequence from *hagA*, designated *HArep3*.

SEQ ID NO. 20 is the deduced amino acid sequence of the polypeptide encoded by *HArep3*.

5 SEQ ID NO. 21 is the nucleotide sequence of the fourth approximately 1.3 kb repeat sequence from *hagA*, designated *HArep4*.

SEQ ID NO. 22 is the deduced amino acid sequence of the polypeptide encoded by *HArep4*.

SEQ ID NO. 23 is a negative primer at 405 nucleotide (t) upstream of the 5' end of the ST 2 fragment used according to the subject invention.

10 SEQ ID NO. 24 is a positive primer at 529 nt 3' of the ST 2 fragment used according to the subject invention.

SEQ ID NO. 25 is the nucleotide sequence of the entire *hagD* gene.

SEQ ID NO. 26 is the deduced amino acid sequence of a polypeptide encoded by a first open reading frame of the entire *hagD* gene.

15 SEQ ID NO. 27 is the deduced amino acid sequence of a polypeptide encoded by a second open reading frame of the entire *hagD* gene.

SEQ ID NO. 28 is the nucleotide sequence of the hemagglutinin gene designated *hagE*.

SEQ ID NO. 29 is the deduced amino acid sequence of the polypeptide encoded by an open reading frame of the *hagE* gene.

20 Detailed Description of the Invention

The DNA sequences of the present invention comprise structural genes encoding proteins which can be involved in the pathogenesis of bacteria responsible for periodontal disease. The genes of the subject invention can be isolated from the DNA of *Porphyromonas gingivalis*. The genes of the subject invention are further characterized by determination of their nucleotide sequences. After
25 obtaining the DNA, a gene library can be developed and the resulting DNA fragments inserted into suitable cloning vectors which are introduced into a compatible host. Depending on the particular host used, the vector can include various regulatory and other regions, usually including an origin of replication, and one or more promoter regions and markers for the selection of transformants. In general, the vectors will provide regulatory signals for expression, amplification, and for a regulated
30 response to a variety of conditions and reagents.

Various markers can be employed for the selection of transformants, including biocide resistance, particularly to antibiotics such as ampicillin, tetracycline, trimethoprim, chloramphenicol, and penicillin; toxins, such as colicin; and heavy metals, such as mercuric salts. Alternatively, complementation providing an essential nutrient to an auxotrophic host can be employed.

Hosts which may be employed for the production of the polypeptides of the present invention include unicellular microorganisms, such as prokaryotes, *i.e.*, bacteria; and eukaryotes, such as fungi, including yeasts, algae, protozoa, molds, and the like. Specific bacteria which are susceptible to transformation include members of the Enterobacteriaceae, such as strains of *Escherichia coli*; *Salmonella*; Bacillaceae, such as *Bacillus subtilis*; *Pneumococcus*; *Streptococcus*; *Haemophilus influenzae*, and yeasts such as *Saccharomyces*, among others.

The DNA sequences can be introduced directly into the genome of the host or can first be incorporated into a vector which is then introduced into the host. Exemplary methods of direct incorporation include transduction by recombinant phage or cosmids, transfection where specially treated host bacterial cells can be caused to take up naked phage chromosomes, and transformation by calcium precipitation. These methods are well known in the art. Exemplary vectors include plasmids, cosmids, and phages.

Genomic libraries of *P. gingivalis* DNA were constructed in known plasmid expression vectors. For example, the plasmid expression vector, pUC9, contains the pBR 322 origin of replication, the pBR 322 ampicillin resistance gene, and a portion of the *lac Z* gene of *E. coli* which codes for the α -peptide of β -galactosidase. The amino terminus of the *lac Z* gene contains a polylinker region which has multiple unique cloning sites. Transformation of *E. coli* JM109, which is defective in β -galactosidase, with pUC9 complements the bacterial β -galactosidase activity, resulting in the ability of the bacterial cell to metabolize the lactose analog X-GAL to a blue color. Cloned DNA inserted in the polylinker region interrupts the *lac Z* gene of the plasmid. Therefore *E. coli* transformants resulting from recombinant plasmids are unable to metabolize X-GAL and appear as white colonies on X-GAL containing plates.

E. coli clones were isolated which stably exhibited *P. gingivalis* antigen expression. These antigens were detected in intact cells both by filter-binding enzyme immunoassay and ELISA. One of these clones, clone 2, was found to encode a polypeptide with an average molecular weight of greater than 125 kD, seen in polyacrylamide gels and detected by Western blot analysis. This polypeptide was later determined to be greater than 144 kD. The entire *hagA* gene which was originally identified from clone 2 is now determined to encode a 283.3 kD protein. Expression of the *P. gingivalis* antigen in clone 2 occurs either in the presence or absence of IPTG but is enhanced by IPTG stimulation. The expression of the clone 3 antigen was also found to be stimulated by IPTG in the same manner as clone 2.

When antigen-expressing clones were surveyed for functional activities, clones 2, 5, and 7 were able to agglutinate erythrocytes whereas *E. coli* JM109 (pUC9) was not. The restriction maps and Southern blot hybridization of these clones indicated that clone 2 cells contain a *Porphyromonas*

DNA insert different from clones 5 and 7. Clone 5, which is also able to autoagglutinate, has a 760 bp DNA fragment in addition to a 4,800 bp fragment in common with the clone 7 insert. Subcloning of these two fragments in different orientations revealed that the 4,800 bp DNA encoded for the hemagglutinating activity and the 760 bp DNA for the autoagglutinating activity. Both fragments must contain a *Porphyromonas* promoter since the subclones with opposite orientations of the inserts still express functional proteins, indicating that antigen expression of clones 5 and 7 is not stimulated by IPTG.

Western blot analysis of clones 5 and 7 and minicell analysis of the subclones further revealed that the *P. gingivalis* DNA fragment encoded polypeptides of approximately 16 kD and approximately 49-50 kD. These polypeptides were sized using SDS-PAGE, under denaturing conditions. A native 49-50 kD protein was also purified by immunoaffinity chromatography. No other purified 49-50 kD protein associated with hemagglutination has been reported. Therefore, the 49-50 kD protein is a previously undetected surface antigen involved in hemagglutination.

E. coli adsorbed rabbit-polyclonal antibody against clone 2 was found to react with several bands in the *P. gingivalis* cell lysate preparation separated by SDS-PAGE. The most rapidly developing and strongest reaction appeared at two bands of 43 kD and 38 kD. Two bands of 32 kD and 30 kD appeared later and three faint bands of 110 kD, 90 kD and 75 kD sometimes were visible still later. This strongly suggests that the *P. gingivalis* hemagglutinin is expressed in clone 2.

E. coli adsorbed rabbit-polyclonal antibody against clones 5 and 7 also reacted with two bands of 43 kD and 38 kD, but barely reacted with the higher bands of 110 kD, 90 kD, and 75 kD, and did not react with the bands of 32 kD and 30 kD. Thus, clones 5 and 7 contain DNA inserts which are nonhomologous with clone 2 and express different antigenic epitopes, but all function as hemagglutinin. The clone 7 insert contains a *Porphyromonas* promoter but the clone 2 insert does not. An *E. coli* host (clone 2) has been designated *E. coli* pST 2 and deposited with the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, MD 20852. Also, an *E. coli* host (clone 5) has been designated *E. coli* pST 5 and it, too, has been deposited with the ATCC. These deposits were assigned the following accession numbers:

	<u>Culture</u>	<u>Accession number</u>	<u>Deposit date</u>
30	<i>E. coli</i> pST 2	ATCC 67733	June 24, 1988
	<i>E. coli</i> pST 5	ATCC 67734	June 24, 1988

The subject cultures have been deposited under conditions that assure access to the cultures will be available during the pendency of this patent application to one determined by the

Commissioner of Patents and Trademarks to be entitled thereto under 37 CFR 1.14 and 35 U.S.C. 122. The deposits are available as required by foreign patent laws in countries wherein counterparts of the subject application, or its progeny, are filed. However, it should be understood that the availability of a deposit does not constitute a license to practice the subject invention in derogation of patent rights granted by governmental action. Further, the subject culture deposits will be stored and made available to the public in accord with the provisions of the Budapest Treaty for the Deposit of Microorganisms, *i.e.*, they will be stored with all the care necessary to keep them viable and uncontaminated for a period of at least five years after the most recent request for the furnishing of a sample of a deposit, and in any case, for a period of at least 30 (thirty) years after the date of deposit or for the enforceable life of any patent which may issue disclosing the cultures. The depositor acknowledges the duty to replace a deposit should the depository be unable to furnish a sample when requested. All restrictions on the availability to the public of the subject culture deposits will be irrevocably removed upon the granting of a patent disclosing them.

The novel genes disclosed and claimed herein can be probed out of the *E. coli* strains which have been deposited with the ATCC. The isolation of these genes can be performed using techniques which are well-known in the molecular biology art. The isolated genes can be inserted into appropriate vehicles which can then be used to transform another microbe.

It is well understood in the field of biotechnology that the subject genes and gene products have many valuable uses. For example, the genes themselves, and fragments thereof, which comprise particular nucleic acid sequences can be used to specifically and selectively hybridize to, or probe, other nucleic acid sequences to determine the presence of homologous sequences therein. This use of the subject nucleotide sequences, or fragments thereof, as probes can have advantageous applications in their use as a diagnostic tool, identifying organisms or other transformants that have nucleic acid sequences which are sufficiently homologous such that, using standard procedures and conditions, hybridization can occur between the test sequences and the probe. As used herein, substantial sequence homology refers to homology which is sufficient to enable the variant to function in the same capacity as the original probe. Preferably, this homology is greater than 50%; more preferably, this homology is greater than 75%; and most preferably, this homology is greater than 90%. The degree of homology needed for the variant to function in its intended capacity will depend upon the intended use of the sequence. It is well within the skill of a person trained in this art to make mutational, insertional, and deletional mutations which are designated to improve the function of the sequence or otherwise provide a methodological advantage.

In addition, the subject nucleotide and fragments thereof can be sequences useful as primers in the preparation and manufacture of sequences by polymerase chain reaction (PCR), inverse

polymerase chain reaction (IPCR), or other nucleic acid synthesis methods. Obviously, the subject genes and fragments can be useful for the production of the gene product, *i.e.*, the antigen or polypeptides encoded thereby.

5 Mutations, insertions, and deletions can be produced in a given polynucleotide sequence in many ways, and these methods are known to the ordinary skilled artisan. Other methods may be come known in the future.

The known methods include, but are not limited to:

- (1) synthesizing chemically or otherwise an artificial sequence which is a mutation, insertion or deletion of the known sequence;
- 10 (2) using a probe of the present invention to obtain via hybridization a new sequence or a mutation, insertion or deletion of the probe sequence; and
- (3) mutating, inserting or deleting a test sequence *in vitro* or *in vivo*.

15 It is important to note that the mutational, insertional, and deletional variants generated from a given probe may be more or less efficient than the original probe. Notwithstanding such differences in efficiency, these variants are within the scope of the present invention. Thus, mutational, insertional, and deletional variants of the disclosed sequences can be readily prepared by methods which are well known to those skilled in the art. These variants can be used in the same manner as the instant probes so long as the variants have substantial sequence homology with the probes.

20 The gene products can also have a variety of uses. For example, the antigens so produced by a gene in a transformed host can be useful in the production of antibodies to the antigen. Those antibodies can be used as probes, when labeled, or can be used in affinity separation techniques. These polypeptides can also be useful as molecular weight markers in chromatographic or electrophoretic procedures, or the like, where molecular weights are used to characterize an unknown polypeptide or identify or confirm the existence of a known polypeptide.

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Following are examples which illustrate materials, methods and procedures, including the best mode, for practicing the invention. These examples are illustrative and should not be construed as limiting.

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Example 1 - Preparation of chromosomal DNA

Porphyromonas gingivalis 381 obtained from a stock culture was grown on plates containing Trypticase soy agar (MBL Microbiology Systems, Cockeysville, MD) supplemented with sheep blood (5%), hemin (5 µg/ml), and menadione (5 µg/ml). The organism was also grown in 10

ml of Todd-Hewitt broth (BBL) supplemented with hemin (5 µg/ml), menadione (5 µg/ml) and glucose (2 mg/ml). Cultures were incubated in an anaerobic chamber in a N₂-H₂-CO₂ (85:10:5) atmosphere at 37°C until the log phase of growth was obtained. The 10 ml broth culture was transferred into 25 ml of the same medium and subsequently transferred to 500 ml of medium. Incubation was at 37°C anaerobically until a late log phase culture was obtained. *E. coli* JM109 [rec A1, end A1, gyr A96, thi, hsd R17 sup E44, rel A1, (lac-pro AN), (F;tra D36, proAB, lac IZ M15)] and the plasmid expression vector pUC9 have been described previously (Viera, J., J. Messing [1982] "The pUC Plasmids, an M13 mp 7-Derived System for Insertion Mutagenesis and Sequencing with Synthetic Universal Primers," *Gene* 19:259-268). *E. coli* JM109 was cultured in Luria-Bertani (LB) medium consisting of Bacto-tryptone (10 g/l), Bacto-yeast extract (5 g/l), and NaCl (5 g/l). For solid media, Bacto-agar was added at a final concentration of 15 g/l. *E. coli* JM109 transformants were selected and maintained on LB plates containing 50 µg of ampicillin/ml.

Next, chromosomal DNA from *P. gingivalis* 381 was prepared as follows: One to three liters of cells were pelleted by centrifugation and washed once with 1x SSC buffer (0.87% NaCl, 0.04% sodium citrate) containing 27% sucrose and 10 mM ethylenediaminetetraacetic acid (EDTA). The cells were pelleted and resuspended in 1/50 of the original volume of the same buffer at 4°C. Lysozyme (5 mg/ml) in SSC was added to 0.5 mg/ml; the mixture was mixed thoroughly and incubated at 37°C for 10 minutes. Nine volumes of 1% SSC containing 27% sucrose 10 mM EDTA and 1.11% SDS (prewarmed to 39°C) were added and the cell suspension was incubated at 37°C for 10 to 30 minutes until cell lysis was complete. In order to denature any contaminating proteins, proteinase K was added to a final concentration of 1 mg/ml and the lysate was incubated at 37°C for 4 hours. DNA was extracted twice with phenol, twice with phenol-chloroform (1:1 by volume), and four times with chloroform. Two volumes of absolute alcohol were added and the precipitated DNA was spooled onto a glass rod. The purified DNA was rinsed with 70% ethanol and suspended in TE buffer, pH 8.0 (10 mM Tris-HCl pH 8.0, 1 mM EDTA).

Alternatively chromosomal DNA was isolated from *P. gingivalis* 381 by a method of CTAB (hexadecyltrimethyl ammonium bromide)/CsCl ultracentrifugation. Briefly, 0.4-0.5 g wet cells was resuspended in 9.5 ml TE buffer (10 mM Tris/Cl, pH 8.0, 1 mM EDTA, pH 8.0), and then 0.5 ml of 10% SDS, and 50 µl of 20 mg/ml proteinase K were added and incubated for 1 hour at 37°C. Then 1.8 ml of 5 M NaCl and 1.5 ml CTAB/NaCl were added and incubated 20 minutes at 65°C. The mixture was extracted with Chloroform/isoamyl alcohol and precipitated with 0.6 volume isopropanol. DNA pellet was dissolved in 20 ml TE buffer and 20 g CsCl and 500 µl of 10 mg/ml ethidium bromide were added and centrifuged 30 minutes at 12,000 rpm using a Beckman GA-20 rotor. The supernatant was then centrifuged in a Beckman VTi50 rotor for 18 hours at 45,000 rpm.

DNA band was collected under long wave UV lamp and ethidium bromide was removed by water saturated butanol extraction and dialyzed against TE buffer thoroughly to remove CsCl.

Chromosomal DNA from the *P. gingivalis* strain W12 can be obtained by similar methods.

5 Example 2 - Isolation of Plasmid DNA and Construction of Genomic Libraries

Plasmid DNA was isolated by the method of Ish-Horowicz and Burke (Ish-Horowicz, D., J.F. Burke [1981] "Rapid and Efficient Cosmid Cloning," *Nucleic Acids Res.* 9:2989-2998) in which cells were lysed with SDS-EDTA in the presence of NaOH. Potassium acetate, pH 4.8, was added at 4°C and cell debris, protein, RNA, and chromosomal DNA were removed by centrifugation. The plasmid was precipitated with two volumes of ethanol, washed with 70% ethanol, dried, and resuspended in TE buffer at pH 7.5. The plasmid was separated from contaminating RNA and any remaining chromosomal DNA by cesium chloride density centrifugation in the presence of ethidium bromide. Ethidium bromide and cesium chloride were removed by butanol extraction and dialysis, respectively. The dialyzed plasmid was then phenol-chloroform extracted, ethanol precipitated, and resuspended in TE buffer.

Purified *P. gingivalis* DNA was then partially digested with *Sau3A* restriction endonuclease to create fragments of 2-10 kilobases which were ligated to the dephosphorylated *Bam*HI site of vector pUC9 with T₄ DNA ligase by standard methods (Maniatis, T., E.F. Fritsch, J. Sambrook [1982] *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY; Sambrook, J., E.F. Fritsch, T. Maniatis [1989] *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY; and Wizard Mini-Prep Kit, Promega Co., Madison, WI). Genomic fragments were also obtained by partial digestion of the chromosomal DNA with *Hind*III restriction endonuclease and ligated to the dephosphorylated *Hind*III site of pUC9. The recombinant plasmids were used to transform *E. coli* JM109. *E. coli* JM109 was grown to an early log phase ($OD_{550} = 0.2$) in LB broth. Ten ml of the culture were centrifuged at 5,000 rpm, for 5 minutes at 4°C and resuspended in 2 ml of transformation buffer 1 (TFM 1, 10 mM Tris-HCl, pH 7.5, 0.15 M NaCl). The cells were then pelleted and resuspended in 2 ml of TFM 2 (50 mM CaCl₂) and incubated on ice for 45 minutes. The cells were again pelleted and gently resuspended in 3 ml of TFM 2, and dispensed into 0.2 ml aliquots. One-tenth ml of TFM 3 (10 mM Tris-HCl, pH 7.5, 50 mM CaCl₂, 10 mM MgSO₄) was added to each aliquot followed by varying amounts of DNA. The cells were then allowed to incubate on ice for 45 minutes, and heat shocked at 37°C for 2 minutes. LB broth (0.5 ml) was added and the cell suspension was incubated at 37°C for 1 hour. Finally, the cells were plated on LB agar containing ampicillin (50 µg/ml) and 5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside (X-GAL) (200 µg/ml) and incubated for 24 to

48 hours at 37°C. All transformants were stored at -70°C in LB broth with ampicillin (50 µg/ml) and 20% glycerol.

Example 3 - Preparation of Antisera and Assay of Antibody Titer

5 Late exponential phase cells of *P. gingivalis* strain 381 were pelleted, washed with 0.01 M phosphate-buffered saline (PBS) pH 7.2, and resuspended in PBS and 0.01 sodium azide at 4°C for at least 1 hour. The cells were again washed with PBS, resuspended to a concentration of 1×10^9 cells/ml and emulsified in an equal volume of Freund's incomplete adjuvant. The cell emulsion was injected in 3 doses at two week intervals for 4 weeks subcutaneously in the back of adult New Zealand rabbits. Each rabbit was given a booster dose 50 to 60 days later. Antisera were collected from the marginal ear veins just prior to immunization and beginning one week after the booster dose. All sera were stored at -20°C.

10 Rabbit anti-*P. gingivalis* antiserum was adsorbed 4 times with *E. coli* JM109 harboring pUC9 plasmid [*E. coli* JM109 (pUC9)]. For each adsorption, *E. coli* cells from 1 liter of a stationary phase culture were washed and mixed with 3 ml of serum at 4°C for 1 hour. The serum was recovered by pelleting the cells at 5,000 xg for 20 minutes. For sonicate adsorption, *E. coli* cells from 500 ml of stationary phase growth suspended in 5 ml PBS were disrupted by sonication and mixed with *E. coli* cell-adsorbed serum for 1 hour at 4°C. The mixture was centrifuged at 100,000 xg for 1 hour and the resulting clear serum was stored at -20°C.

15 Sera were then tested for anti-*P. gingivalis* and anti-*E. coli* activities by an enzyme-linked immunosorbent assay (ELISA). *P. gingivalis* cells suspended in carbonate-bicarbonate buffer, pH 9.6 (10^8 cells per well) were fixed to microtiter plates at 4°C overnight. After the wells were washed with 0.5% "TWEEN-20" in PBS, 1% bovine serum albumin (BSA) in PBS was added to each well, and the plates were incubated for 2 hours at room temperature in order to saturate the binding sites.

20 After washing the plates, serially diluted antiserum was added and plates were incubated for 1 hour at room temperature followed by a second wash with 0.5% "TWEEN-20" in PBS. Peroxidase conjugated goat anti-rabbit IgG, diluted 1:1000 in 1% BSA, was added and the plates were again incubated at room temperature for 1 hour. After a final washing, a color-forming substrate solution (0-phenylenediamine, 0.5 g/100 ml in 0.1 M citrate buffer, pH 4.5, and 1.8% hydrogen peroxide)

25 was added, and the plates were incubated for 30 minutes at room temperature. The absorbance at 492 nm was measured with a Titertek Multiscan reader. An absorbance of 0.05 or more over background was considered positive. Background readings were obtained from the wells in which all reagents except anti-*P. gingivalis* antiserum was added. Normal rabbit serum was also tested

30

against *P. gingivalis* antigen. To test the effectiveness of adsorption, the titers of treated sera were assayed as described above except that *E. coli* JM109 (pUC9) whole cells were used as the antigen.

It was found that rabbit anti-*P. gingivalis* antiserum had an antibody titer of 1:64,000 to *P. gingivalis* and 1:160 to *E. coli* (pUC9), whereas normal rabbit serum had an antibody titer of 1:10 to *P. gingivalis* and 1:80 to *E. coli* (pUC9). Adsorption of anti-*P. gingivalis* antiserum with *E. coli* (pUC9) resulted in a slight reduction of antibody titer to *P. gingivalis* and reduced the anti-*E. coli* titer to zero or 1:10.

Example 4 - Filter-Binding Enzyme Immunoassay

Ampicillin-resistant transformants which formed white colonies in the presence of X-GAL were spotted onto LB agar plates with ampicillin, grown overnight, and blotted onto nitrocellulose filter disks. *P. gingivalis* and *E. coli* JM109 (pUC9) were also spotted onto each filter as a positive and negative control, respectively. Duplicate prints of the colonies on nitrocellulose filters were made and colonies on one of each duplicate print were lysed by a 15-minute exposure to chloroform vapor. Filters were then air dried for 30 minutes and soaked for 2 hours in PBS containing 3% BSA. After the filters were washed, adsorbed rabbit anti-*P. gingivalis* antiserum was added and the filters were incubated in a solution of peroxidase conjugated goat anti-rabbit immunoglobulin for 1 hour. After washing, the filters were developed in a color-forming substrate solution consisting of 0.06% 4-chloro-1-naphthol and 3% hydrogen peroxide in a 1:4 solution of methanol-TBS (50 mM Tris hydrochloride, 200 mM NaCl, pH 7.4). Clones which developed a blue color were picked and rescreened by the same procedure.

A total of 1,700 colonies of transformants resulting from *Hind*III restricted chromosomal DNA were tested for the expression of *P. gingivalis* antigens. Seven clones gave positive signals.

Example 5 - Restriction and Southern Blot Analysis of Recombinant Plasmids

To further confirm the positive results of the filter-binding enzyme immunoassay, plasmid DNA was isolated from each positive clone. Electrophoresis of these unrestricted plasmids showed that each clone contained only one recombinant plasmid.

Southern blot analysis was also performed to confirm that the DNA inserts were derived from the *P. gingivalis* DNA. Plasmids were isolated from all the clones that were positive in the filter-binding enzyme immunoassay. Restriction endonuclease digestions were performed under conditions described by the manufacturer to produce complete digestion. Agarose gel electrophoresis was performed as described by Maniatis *et al.* (1982, *supra*).

Recombinant plasmid and pUC9 vector DNAs were digested to completion with the appropriate restriction enzymes and run on a 1.2% agarose gel. *P. gingivalis* DNA partially digested with *Sau3A*, and *HindIII*-digested *Eikenella corrodens* clone 18 DNA were also loaded in the gel. The DNA was transferred to "BIODYNE" nylon membrane by Southern transfer (Southern, E.M. [1975] "Detection of Specific Sequences Among DNA Fragments Separated by Gel Electrophoresis," *J. Mol. Biol.* 98:503-517). *P. gingivalis* DNA partially digested with *HindIII* was nick translated with (α -³²P dCTP) (400 Ci/mmol, Amersham Corp., Arlington Heights, Ill.) as described by Maniatis *et al.* (1982, *supra*). The membrane-bound DNA was hybridized to the nick-translated probe at 42°C in 50% formamide for 16 hours by the method recommended by the manufacturer (Pall Ultrafine Filtration Corp., Glen Cove, NY) which was adapted from Wahl *et al.* (Wahl, G.M., M. Stern, G.R. Stark [1979] "Efficient Transfer of Large DNA Fragments from Agarose Gels to Diazobenzyloxy-Methyl-Paper and Rapid Hybridization by Using Dextran Sulfate," *Proc. Natl. Acad. Sci. USA* 76:3683-3687). The membrane was washed at room temperature in wash buffer (2 x SSC and 0.1% SDS) four times each for 5 minutes and twice at 50°C each for 15 minutes in 0.1 x SSC, 0.1% SDS. An autoradiogram was obtained with Kodak XAR-5 film (Eastman Kodak Co., Rochester, NY) and Cronex Quanta II intensifying screen (DuPont Co., Wilmington, DE).

Clones 1, 2, 4, 5, 7, and 8 were generated from *HindIII*-restricted chromosomal DNA. After digestion with *HindIII*, only clones 5, 6, 7, and 8 revealed fragments of the linear pUC9 vector and fragments of *P. gingivalis* DNA inserts. Plasmid DNAs of these clones were restricted with various enzymes and analyzed by gel electrophoresis. The estimated size of inserts of clones 5, 6, 7, and 8 are 5.5, 5.5, 4.8, and 3.5 kb, respectively (Table 1). Thus clones 5 and 6 were found to contain plasmids of the same size and identical restriction fragments.

Clone 3, which was constructed by ligation of *Sau3A* partially digested *P. gingivalis* DNA with *BamHI* cut pUC9, was restricted with *SmaI* and *SalI*. Restriction analysis revealed a fragment of linear 9 bp-deleted pUC9 and 2 fragments of insert. Restriction analysis with different enzymes showed that the size of the insert of clone 3 was approximately 1.1 kb.

Although clones 1, 2, and 4 were generated from *HindIII* restricted DNA, they did not result in fragments of linear pUC9 after *HindIII* digestion. These cloned DNAs were then restricted with *PvuII*, which generates a 307 bp fragment containing the polylinker-cloning sites from pUC9. Clones 1, 2 and 4 revealed fragments of linear 307 bp-deleted pUC9 and inserts associated with the deleted fragment. These cloned DNAs were digested with various restriction enzymes and analyzed by agarose gel electrophoresis. The size of inserts of clones 1, 2, and 4 were found to be 3.2, 3.2,

and 3.3 kb, respectively (Table 1). Clones 1 and 2 also contained plasmids of the same size and identical restriction fragments.

Table 1. Characterization of *E. coli* transformants which express *P. gingivalis* antigens

Clone No.	Colonies reacted with antiserum		Size of <i>B. gingivalis</i>
	unlysed	lysed	DNA cloned (Kb)
1 and 2	+	+	3.2
3	+	+	1.1
4	+	+	3.3
5 and 6	+	+	5.5
7	+	+	4.8
8	- ^b	+	3.5

^a = Positive reaction

^b = Negative, not reactive

Example 6 - Assay of the Titer of Anti-*P. gingivalis* Antiserum to *E. coli* Transformants Which Express *P. gingivalis* Antigens

Cultures of each representative clone were prepared by 100-fold dilution of overnight cultures and grown for 2 hours at 37°C. Isopropyl-β-D-thiogalactopyranoside (IPTG) was added to specific cultures at a final concentration of 1 mM and the cells were pelleted by centrifugation 4 hours later. The cells were washed, resuspended in 1/10 volume of PBS, and the optical density of each suspension was determined at 550 nm. Cell lysate antigen was prepared by breaking the cells with a sonicator. The protein concentration of each lysate was determined by the Bio-Rad protein assay (Bio-Rad Laboratories, Richmond, CA). Determination of the titer of anti-*P. gingivalis* 381 against these antigens was performed with the ELISA as described above (10⁸ cells or 1 μg protein per well). Normal rabbit serum exhaustively adsorbed with *E. coli* JM109 (pUC9) was also tested in the same manner.

Anti-*P. gingivalis* antiserum was able to detect antigen expression in all positive clones except clone 8 in an enzyme-linked immunosorbent assay (ELISA). The antiserum reacted with both whole cell and cell lysate antigens. Isopropyl-β-D-thiogalactopyranoside (IPTG) was not necessary to induce antigen expression. However, in the presence of IPTG, clones 2 and 3 showed higher antigen expression, especially when the cell lysate preparations were tested. These results are shown in Table 2.

Table 2. Titer of anti-*P. gingivalis* antiserum against *E. coli* transformants which express *P. gingivalis* antigens

Organism	Antibody titers ^a against test antigens ^b			
	Whole cell		Cell Lysate	
	IPTG ⁻	IPTG ⁺	IPTG ⁻	IPTG ⁺
Clone 1	320	NT ^c	320-640	NT
Clone 2	320	640	320-640	1280-2560
Clone 3	20	160	40-160	1280
Clone 4	20-100	20-40	20-40	20-40
Clone 5	40-80	40-80	40-80	40-80
Clone 6	40	NT	40	NT
Clone 7	40	40	40	40
Clone 8	0	0	0	NT
<i>E. coli</i> JM109 (pUC9)	0-10	0-10	0-10	0-10
<i>P. gingivalis</i>	40,960-64,000	NT	NT	NT
Control NRS ^d				

^aNumber designates the reciprocal dilution of the sera which gave OD₄₉₂ reading of 0.05 or more over the background. Antiserum was exhaustively adsorbed with *E. coli* JM109 (pUC9).

^bAntigens were prepared from cultures grown without IPTG (IPTG⁻) or in the presence of IPTG (IPTG⁺).

^cNot tested.

^dNormal rabbit serum exhaustively adsorbed with *E. coli* JM109 (pUC9) did not react to test antigens.

Example 7 - Sodium Dodecyl Sulfate - Polyacrylamide Gel Electrophoresis (SDS-PAGE)

Five stable representative clones were analyzed for antigen expression by SDS-PAGE. Each of the representative antigen-producing clones was grown to mid-log phase in 3.0 ml of LB broth with 50 µg of ampicillin/ml. The cells were pelleted, washed with PBS, resuspended in 0.3 ml of sample buffer (62.5 mM Tris-hydrochloride, 5% 2-mercaptoethanol, 2% SDS, 10% glycerol, 0.002% bromphenol blue, pH 6.8), and boiled for three minutes. The *P. gingivalis* cell lysate was mixed with an equal volume of sample buffer and treated in the same manner.

SDS-PAGE was performed using a 12% polyacrylamide gel in a vertical slab gel electrophoresis tank (Hoefer Scientific Instruments, San Francisco, CA) as described by Laemmli (Laemmli, U.K. [1970] "Cleavage of Structural Proteins During the Assembly of the Head of Bacteriophage T4," *Nature* (London) 227:680-685). A whole cell preparation from clone 2 was

separated in a 5% SDS polyacrylamide gel and the expressed protein was initially estimated to have a molecular weight of more than 125 kD and later determined to be greater than 144 kD.

Example 8 - Assay for Removal of SHA Adherence Inhibition by Anti-*P. gingivalis* Antiserum

5 The expression of components detected by *in vitro* methods was subjected to further examination. The antigen-expressing clones described in the previous examples were tested for the expression of adhesins for saliva-treated hydroxyapatite (SHA adhesin). Anti-*P. gingivalis* 381 antiserum which inhibits the adherence of *P. gingivalis* 381 to SHA was adsorbed with each antigen-expressing clone until the titer of the antiserum to each clone was reduced to zero. Each adsorbed
10 antiserum was tested for inhibition of *P. gingivalis* adherence to SHA.

Porphyromonas gingivalis 381 was cultured in Todd-Hewitt broth. *E. coli* transformants were cultured in LB medium containing 50 µg of ampicillin/ml by preparing 100-fold dilutions of overnight cultures followed by incubation for 2 hours at 37°C. IPTG was added to the cultures, when used at a final concentration of 1 mM, and the cultures were incubated for an additional 4
15 hours.

 An assay for the removal of SHA adherence inhibition using anti-*P. gingivalis* antiserum was used to test for SHA adherence. In order to do this, aliquots of anti-*P. gingivalis* antiserum were adsorbed with each antigen-expressing clone as well as *E. coli* JM109 (pUC9). The titer of each adsorbed antiserum was tested against each clone and *P. gingivalis* whole cell antigen by ELISA as
20 described above.

 Whole paraffin-stimulated human saliva was collected and heated at 56°C for 30 minutes to inactivate degradative enzymes. Extraneous debris and cells were removed by centrifugation at 12,000 rpm for 10 minutes and sodium azide was added to a final concentration of 0.04%.

 Hydroxyapatite (HA) beads (BDH Biochemical, Lt., Poole, England) were treated as
25 previously described (Clark, W.B., L.L. Bammann, R.J. Gibbons [1978] "Comparative Estimates of Bacterial Affinities and Adsorption Sites on Hydroxyapatite Surfaces," *Infect. Immun.* 19:846-853). Briefly, 10 mg of beads were washed and hydrated in distilled water in 250 µl plastic microfuge tubes followed by equilibrium overnight with adsorption buffer (0.05 M KCl, 1 mM K_2HPO_4 , pH 7.3, 1 mM $CaCl_2$ and 0.1 mM $MgCl_2$). The beads were incubated with 200 µl of saliva
30 for 24 hours at 4°C and then washed with sterile adsorption buffer to remove nonadsorbing material. Control tubes without HA were treated identically.

P. gingivalis 381 cells were labeled by growth to late log phase in medium supplemented with (3H) thymidine (10 mCi/ml). The cells were pelleted, washed twice in adsorption buffer, and dispersed with three 10-second pulses (medium power) with a microultrasonic cell disrupter.

The dispersed cells were mixed with each antiserum (1:100 dilution) and normal rabbit serum to a final concentration of 4×10^6 cell/ml. The cell-antiserum suspensions (200 μ l) were then added to the SHA beads in microfuge tubes and the tubes were rotated in an anaerobic chamber for 1 hour. Labeled cells alone (no antisera) were treated in the same manner to determine the number of cells adhering to the SHA surface. A control tube containing cells but no SHA was tested to quantitate the amount of cells bound to the tubes rather than to the SHA. One hundred microliters of adsorption buffer containing unadhered cells was removed and placed in minivials containing 3 ml of aqueous scintillation cocktail (Amersham/Searle, Arlington Heights, IL), and counted with a scintillation counter (Model 455 Packard Tricarb). Determination of the number of cells adhering to the SHA was done by subtracting the number of cells (no. of counts) in solution from the total number of cells (no. of counts) which did not adhere to the tube.

The results in Table 3 summarize the SHA inhibition data and indicate that the antiserum adsorbed with each antigen-expressing clone still inhibited the adherence of *P. gingivalis*.

Table 3. Inhibition of adherence to SHA by adsorbed anti-*P. gingivalis*

Inhibitor and dilution		% adherence ^a	% inhibition ^b
None		83.85	-
Normal rabbit serum	1:100	80.08	0.05
Antiserum unadsorbed	1:100	22.70	72.15
Antiserum adsorbed with:			
<i>E. coli</i> JM109 (pUC9)	1:100	21.57	73.07
Clone 2	1:100	10.73	86.59
Clone 3	1:100	22.60	71.78
Clone 4	1:100	16.24	79.71
Clone 5	1:100	27.37	65.82
Clone 7	1:100	19.90	75.15

^aPercent adherence was calculated from the following formula: % adherence = [(cpm from tube without SHA - cpm from tube with SHA)/(cpm from tube without SHA)] x 100.

^bPercent inhibition was calculated from the following formula: % inhibition = [1 - (% adherence in the presence of antibody / % adherence in the absence of antibody)] x 100.

Example 9 - Direct Hemagglutination Assay

The rationale to identify the clones which express hemagglutinin were analogous to those described for the SHA adhesin. The anti-*P. gingivalis* antiserum adsorbed with each antigen-expressing clone and *E. coli* JM109 (pUC9), as described for the SHA assay, were tested for removal of hemagglutination inhibition activity of anti-*P. gingivalis* antiserum. Since it is necessary

to determine the minimum number of *P. gingivalis* cells which produce hemagglutinin before performing the hemagglutination inhibition assay, a direct hemagglutination assay of antigen-expressing clones together with *P. gingivalis* was first performed.

5 A direct hemagglutination assay was used to test for adhesion to erythrocytes. The hemagglutination assays were carried out in V-bottom microtiter plates (Dynatech Laboratories, Inc., Alexandria, VA). Erythrocytes (sheep or human group O) were washed three times with PBS (0.02 M phosphate buffered saline), pH 7.2, and resuspended to a final concentration of 0.2% (v/v). Cells of *P. gingivalis* and antigen-expressing clones were washed twice in PBS and resuspended to an optical density of 0.5 and 2.0, respectively, at 660 nm. The cell suspensions were diluted in a
10 twofold series with PBS and 0.05 ml of the suspensions were added to the wells. *E. coli* JM109 (pUC9), which was prepared in the same manner as the antigen-expressing clones, was included as a control. An equal volume (0.05 ml) of washed erythrocytes was added and mixed with the bacterial cells. The plates were stored for 16 hours at 4°C and then examined for evidence of hemagglutination as follows. Agglutinated erythrocytes will settle as clumps which will be dispersed
15 throughout the bottom of the wells, resulting in a pinkish-red coating of each well. In the absence of hemagglutination, the erythrocytes will settle on the bottom of the well as a central, smooth, bright red round disk. The titer was expressed as the reciprocal of the highest dilution showing positive agglutination.

The hemagglutination inhibition assay was also carried out in V-bottom microtiter plates.
20 *P. gingivalis* cell suspensions in PBS were adjusted to the optical density of 0.5 at 660 nm. Each antiserum examined for hemagglutination inhibition activity was diluted twofold in a series of wells. Fifty microliters of the bacterial suspension containing twice the minimum number of cells which produced hemagglutination was then added to each well. After incubation with gentle shaking at room temperature for 1 hour, 0.05 ml of the washed erythrocytes were added to each well and mixed.
25 The plates are left for 16 hours at 4°C and read for hemagglutination as described above for the hemagglutination assay. The titer was expressed as the reciprocal of the highest dilution showing hemagglutination inhibition.

E. coli transformants which were able to agglutinate erythrocytes were grown in LB broth containing ampicillin as described above. Two rabbits were injected with each clone as previously
30 described. Sera were exhaustively adsorbed with *E. coli* JM109 (pUC9) and tested for anti-*P. gingivalis* activity by ELISA.

Anti-clone 2 antiserum diluted 1:10 was separately adsorbed with *P. gingivalis*, *E. coli* JM109 (pUC9), and clones 2, 5, and 7. Washed stationary phase cells of each bacterial culture were prepared as described above. For each adsorption, 10^7 , 10^8 , 10^9 and 10^{10} bacterial cells were mixed

with 200 µl of serum and the suspensions were stored at 4°C overnight. The sera were recovered by centrifugation at 12,000 xg for 10 minutes. Each adsorbed antiserum was assayed by ELISA to determine the titer to *P. gingivalis*.

5 The direct hemagglutination assay of these clones demonstrated that clones 2, 5, and 7 did agglutinate sheep erythrocytes, whereas *E. coli* JM109 (pUC9) did not. The hemagglutination titer of clone 2 was 2 and that of clones 5 and 7 agglutinated erythrocytes at the undiluted suspension. In addition, clone 5 was found to auto-agglutinate when resuspended in PBS, pH 7.2.

Example 10 – DNA Restriction Mapping and Characterization Procedures

10 Restriction endonuclease digestions of the recombinant plasmids from clones 2, 5, and 7 were performed according to manufacturer's directions. Clone 5 DNA was digested with *Hind*III and two fragments of *P. gingivalis* inserts were isolated from agarose gels by the method of Zhu *et al.* (Zhu, J.W. Kempenaers, D. Van der Straeten, R. Contreras, W. Fiers [1985] "A Method for Fast and Pure DNA Elution from Agarose Gels by Centrifugal Filtration," *Biotech.* 3:1014-1016) employing
15 centrifugal filtration of DNA fragments through a Millipore membrane inside a conical tip. The DNA preparations were extracted with phenol-chloroform, precipitated with ethanol and resuspended in TE, pH 8.0. Each DNA fragment was ligated to *Hind*III-digested pUC9 and the resulting recombinant plasmids were transformed into competent *E. coli* JM109 cells as described previously. Recombinant plasmids from these transformants were isolated by rapid plasmid DNA isolation
20 (Silhavy, T.J., M.L. Berman, L.W. Enquist [1984] *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY), digested with appropriate restriction endonucleases, and analyzed by agarose gel electrophoresis.

The recombinant plasmids of clones, 2, 5, and 7 were restricted with several restriction endonucleases and analyzed in 1.2% agarose gels. A schematic diagram of restriction enzyme
25 recognition sites of these three clones is detailed in Figure 1. These data show that the clone 2 insert is different from that of clones 5 and 7, whereas clones 5 and 7 have one insert fragment in common. The restriction map of clone 2 revealed that the *Hind*III site of the DNA insert at the amino terminal end of the β-galactosidase gene was still intact, but a deletion occurred at the other end of the insert and included most of the linker. The linker region with recognition sites of *Pst*I, *Sal*I, *Bam*HI and
30 *Sma*I was deleted but the *Eco*RI site was still intact as well as other sites upstream such as *Pvu*II and *Nar*I.

To further confirm the results of the restriction maps, ³²P-labeled clone 7 recombinant DNA was used as a probe for hybridization of restricted recombinant plasmids by Southern blot analysis. Clone 2 DNA restricted with *Hind*III, *Eco*RI, and *Sma*I resulted in DNA fragments of pUC9 and four

pieces of insert of approximately 1,400, 1,300, 420, and 150 bp. Clone 5 DNA restricted with *HindIII* resulted in fragments of pUC9 and two pieces of insert approximately 4,800 and 760 bp. Fragment bands of pUC9 and inserts of approximately 2,800, 2,000, and 760 bp were generated from digestion of clone 5 DNA with *HindIII* and *BamHI*. Clone 7 DNA restricted with *HindIII* alone and *HindIII* together with *BamHI* resulted in pUC9 and an insert of 4,800 bp, and pUC9, insert of 2,800 and 2,000 bp, respectively.

Hybridization of these transferred restricted DNAs demonstrated that the clone 7 probe hybridized to pUC9 and the common insert of clones 5 and 7 but not to the insert of clone 2.

Clone 5 was found to agglutinate erythrocytes and autoagglutinate, while clone 7 was only able to agglutinate erythrocytes. Clone 5 has an insert of 760 bp in addition to the common insert of 4,800 bp of clone 7. This data suggested that the 760 bp insert might encode for the autoagglutinating activity and the 4,800 bp fragment for the hemagglutinating activity of clone 5. The recombinant plasmid of clone 5 was thus digested with *HindIII* to generate pUC9 and inserts of 4,800 and 760 bp. Each insert band was isolated from these transformants and digested with restriction endonucleases. Subclones with different orientations of the insert were obtained. Subclones of 760 bp inserts were designated clone 5.1 and 5.2 and the subclones of 4,800 bp inserts, clone 5.3 and 5.4. Recombinant plasmids of clones 5.1 and 5.2 digested with *HindIII* did result in pUC9 and the 760 bp inserts, and different patterns of restricted DNAs were seen when digested with *SalI*. *HindIII*-restricted recombinant plasmids of clones 5.3 and 5.4 revealed pUC9 and inserts of 4,800 bp, while *EcoRI*-restricted recombinant plasmids showed different patterns. Both clones 5.1 and 5.2 were able to autoagglutinate when resuspended in PBS, pH 7.2, but could not agglutinate erythrocytes. Clones 5.3 and 5.4 were both able to agglutinate erythrocytes but did not autoagglutinate.

Example 11 - Identification and Characterization of Gene Products by Sodium Dodecyl Sulfate-Polyacrylamide Gel Electrophoresis (SDS-PAGE), Western Blot, Minicell Analysis, and Immunoaffinity Chromatography

P. gingivalis cell lysate and cells of *E. coli* transformants were prepared and analyzed by SDS-PAGE as described above and Western blot as described by Burnette (Burnette, W.N. [1981] "Western Blotting: Electrophoretic transfer of proteins from sodium dodecyl sulfate-polyacrylamide gels to radiographic detection with antibody and radioiodinated protein A," *Anal. Biochem.* 112:195-203). Antisera to clones 2, 5, and 7 exhaustively adsorbed with *E. coli* JM109 (pUC9) were used as probes in the Western blot. Control antisera included anti-clone 2 antiserum also adsorbed with

P. gingivalis at the ratio of 10^{10} cells per 100 μ l of antiserum, and antiserum to *E. coli* JM109 harboring pUC9 with *Eikenella corrodens* DNA insert.

Upon Western blot analysis of clone 2, a protein antigen of approximately 125 kD and a smear of lower molecular weight were detected using *E. coli* adsorbed anti-*P. gingivalis* antiserum but no corresponding antigens expressed in clones 5 and 7 were detected by Western blot analysis. Clones 5 and 7 did, however, express a protein detected as a major band of approximate M.W. 49-50 kD by Western blot analysis and revealed an additional minor band of 27 kD upon minicell autoradiography.

For the identification of clones 5 and 7 gene products, the minicell procedure was used as described by Clark-Curtiss *et al.* and Dougan *et al.* (Clark-Curtiss, J.E., R. Curtiss III [1983] "Analysis of Recombinant DNA Using *Escherichia coli* Minicells," *Methods Enzymol.* 101:347-362; Dougan, G., M. Kehoe [1984] "The minicell system as a method for studying expression from plasmid DNA," *Methods Microbiol.* 17:233-258). Recombinant plasmids were transformed into *E. coli* as previously described. Transformants were selected on LB plates containing 50 μ g/ml ampicillin and 10 mM isopropyl- β -D-thiogalactopyranoside (IPTG). Colonies were streaked for isolation and grown overnight at 37°C in BSG (phosphate-buffered saline + 0.01% gelatin) containing 50 μ g/ml ampicillin. Minicells were then isolated by sequential low speed centrifugation, high speed centrifugation of the low speed supernatant fluid, and centrifugation through a 5-30% (w/v) sucrose gradient. The sucrose gradient centrifugation was repeated at least once. The minicells were collected and diluted twofold in BSG, pelleted by centrifugation at 10,000 rpm for 10 minutes, and the resulting pellet was resuspended in minicell labeling medium containing no methionine. After incubation of the minicell suspension for 10 minutes at 37°C, 10 μ Ci of 35 S-methionine were added. Following a 15 minute incubation, the cells were chilled for 10 minutes on ice and pelleted by a two minute centrifugation in a microfuge. The cell pellets were then processed for SDS-PAGE. Autoradiography was performed on 35 S-methionine labeled minicell preparations which were electrophoresed on a 12% SDS-PAGE.

In order to determine the native *P. gingivalis* antigens which clone 2 expressed, antisera against clone 2 were made in rabbits for use as a probe in Western blot analysis. Pooled anti-clone 2 antiserum had a titer of 1:16,000 against *P. gingivalis* whole cell antigen. This antiserum was adsorbed exhaustively with *E. coli* JM109 (pUC9) until the anti-*E. coli* titer was reduced from 1:50,000 to 1:10 in the *E. coli* whole cell ELISA. The adsorbed antiserum, diluted to 1:200, was used as a probe to detect antigens separated in a 12.5% SDS polyacrylamide gel and transferred to a nitrocellulose sheet. This antiserum reacted with two major bands of approximately MWs 43,000 and 38,000 and two bands of MWs 32,000 and 30,000 in *P. gingivalis* cell lysate antigen and the

125 kD protein band of expressed antigen in clone 2. Normal rabbit serum reacted to a common 40,000 molecular weight band of all the clones and *E. coli* JM109 (pUC9).

In order to prove that the *P. gingivalis* reactive polypeptides are exclusively *P. gingivalis* proteins, the native *P. gingivalis* antigens were reacted to *E. coli* adsorbed anti-clone 2 antiserum, *P. gingivalis* cell lysate antigen and clone 2 whole cell antigen were again separated in 12.5% SDS-polyacrylamide gel. Upon transfer to a nitrocellulose sheet, each was reacted with (1) *E. coli* adsorbed anti-clone 2 antiserum, (2) *P. gingivalis* adsorbed anti-clone 2 antiserum, and (3) antisera to *E. coli* JM109 harboring pUC9 with an *Eikenella corrodens* DNA insert. *E. coli* adsorbed anti-clone 2 reacted to *P. gingivalis* cell lysate at two major bands of MWs 43,000 and 33,000, two bands of MWs 32,000 and 30,000 and three faint bands of higher molecular weight of approximately 110,000, 90,000 and 75,000 daltons. This adsorbed antiserum also reacted to a band of expressed antigen having a molecular weight greater than 125 kD in clone 2.

To define the native *P. gingivalis* antigens which clones 5 and 7 expressed, antisera against clones 5 and 7 were also made in rabbits and had titers of 1:800 and 1:1,600 to *P. gingivalis* antigens. These antisera exhaustively adsorbed with *E. coli* were used to identify the reactive native *P. gingivalis* antigens. Antisera against clones 5 and 7 at the dilution of 1:5 and 1:10 were found to react with two bands of approximately 43,000 and 38,000 daltons in *P. gingivalis* cell lysate antigen preparation but did not react to the expressed clone 2 antigen. This antiserum also reacted to a common band of approximately 36,000 daltons of *E. coli* antigen in each clone and *E. coli* JM109 (pUC9). Normal rabbit serum did not react to any *P. gingivalis* antigens.

Immunoaffinity chromatography was used to identify and purify the native *P. gingivalis* gene product and to verify that inserts of clones 5 and 7 contained the entire gene. Immune rabbit IgG was purified via DEAE cellulose. Following the precipitation of IgG by the addition of saturated ammonium sulfate to the sera, the IgG was coupled to "AFFI-GEL" (Bio-Rad Laboratories, Richmond, CA) by incubation for two hours at room temperature and overnight at 4°C. The coupled material was then used to prepare a 3 cm³ column. After the column was washed extensively with 0.02 M phosphate buffer, pH 8.0, 1-2 ml of *P. gingivalis* 381 sonicate containing 18 mg/ml protein were added and run through the column using a peristaltic pump generating a flow rate of 20 ml/hr. The column eluate was monitored for absorbance at 280 nm. The column retentate was eluted from the column by addition of 0.1 M glycine, pH 2.5. The recovered retentates were concentrated by centrifugation through a molecular weight cut-off filter, pressure concentration in an Amicon filter (Amicon, Danvers, MA), lyophilization, or a combination of the above. When a *P. gingivalis* 381 cell lysate was applied to an affinity column containing anti-clone 7 rabbit IgG,

and the retained antigenic peptides were eluted and analyzed by SDS-PAGE, a major band at 49-50 kD was evident.

Example 12 - Determination of the Relationship Between the Expressed Antigens of Clones 2, 5 and

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Although antisera against clones 2, 5, and 7 reacted to *P. gingivalis* cell lysate at two major bands of 43,000 and 38,000 MWs, *E. coli* adsorbed anti-clone 2 antiserum also reacted to the greater than 125 kD protein band synthesized in clone 2. However, *E. coli* adsorbed anti-clone 5 and anti-clone 7 antisera did not react to this expressed antigen band of clone 2.

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To further define the relationship of the epitopes of the expressed antigen in clone 2 from that of clones 5 and 7, adsorption of anti-clone 2 antiserum with several antigens was performed and each adsorbed anti-clone 2 antiserum was tested for its titer to *P. gingivalis* whole cell antigen by ELISA. The antibody titer to *P. gingivalis* of anti-clone 2 antiserum was removed in a dose response manner by adsorption with *P. gingivalis* and clone 2 cells. Adsorption with *E. coli* JM109 (pUC9),

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clone 5 or clone 7 did not reduce the antibody titer to *P. gingivalis* of anti-clone 2 antiserum. The ability of antisera to *P. gingivalis* and hemagglutinable *E. coli* to inhibit the hemagglutinating activity of *P. gingivalis* was determined and is summarized in Table 4. All antisera inhibited *P. gingivalis* hemagglutination at titers four to eight times that of normal rabbit sera.

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Table 4. Inhibition of hemagglutinating activity of *P. gingivalis* by anti-hemagglutinating *E. coli* antisera.

Antiserum	Hemagglutination inhibition titer
Anti- <i>P. gingivalis</i>	
unadsorbed	640
adsorbed with <i>E. coli</i> JM109 (pUC9)	640
Normal rabbit serum ^a	160
Anti-clone 2	320-640
Preimmune	80
Anti-clone 5	160
Preimmune	40
Anti-clone 7	160
Preimmune	40

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^aNormal rabbit serum and preimmune sera titers are from each particular group of rabbits.

Example 13 - DNA Sequencing of *P. gingivalis* Hemagglutinin Genes

The *P. gingivalis* 381 chromosome contains at least five genes which encode hemagglutinin. The *P. gingivalis* genes encoding hemagglutinin proteins have been designated *hagA*, *hagB*, *hagC*, *hagD*, and *hagE*. Genes encoding hemagglutinins were cloned using standard procedures as described above or with minor modifications as readily recognized and understood in the art. Plasmid DNA was isolated from the transformed hosts by a rapid method wherein DNA samples for sequencing were prepared by alkaline-lysis/PEG precipitation method. Briefly, transformed *E. coli* JM 109 cells growing in 50 ml Terrific broth with ampicillin were collected (ca. 0.5 g wet weight) and resuspended in 2 ml of 50 mM glucose, 25 mM Tris/Cl (pH 8.0), and 10 mM EDTA (pH 8.0). A freshly prepared 4 ml solution of 0.2 N NaOH, 1% SDS was added and left on ice for 10 minutes. Then 3 ml of ice-cooled potassium acetate solution was added and left on ice for 10 minutes. The mixture was centrifuged 30 minutes at 9,000 rpm at 4°C and RNase A was added to a final concentration of 20 µg/ml to the supernatant and incubated for 20 minutes at 37°C. The mixture was extracted thoroughly with chloroform/isoamyl alcohol. An equal volume of isopropanol was added to precipitate DNA, left for 10 minutes at room temperature, and centrifuged for 30 minutes at 9,000 rpm at room temperature. The DNA pellet was dissolved in 3.36 ml of H₂O. Then 0.64 ml of 5 M NaCl and 4 ml of 13% PEG 8000 (polyethylene glycol, Sigma) were added and left on ice for more than 1 hour. After centrifugation for 15 minutes at 9,000 rpm at 4°C, the DNA pellet was dissolved in sterilized water. By this method, 200 to 400 µg of highly purified plasmid DNA can be obtained in one day.

A. Characterization of the *hagA* gene and gene product. The hemagglutinin gene designated *hagA* was obtained from the *P. gingivalis* 381-derived clone ST 2, and was determined to be more than 4500 bp in length. The sequence of the ST2-derived DNA sequence is shown in SEQ ID NO. 1. The open reading frame (ORF) of the *hagA* gene from clone 2 was determined to encode a polypeptide of at least 1339 amino acids, and >144 kD. The derived amino acid sequence encoded by the *hagA* gene from clone 2 is shown in SEQ ID NO. 2. A 10,119 bp *EcoRV* fragment was cloned that included an additional 338 bp of upstream sequence. The complete open reading frame (ORF) of *hagA* was found to be 7,887 bp in length (bases 365 to 8251 of the *EcoRV* fragment), encoding a protein of 2,628 amino acids with a molecular weight of 283.3 kD. The nucleotide and deduced amino acid sequences of the entire *hagA* gene are shown as SEQ ID NO. 13 and SEQ ID NO. 14, respectively. It was initially found that the *hagA* sequence has an approximately 1.1 kb repeating unit which repeats at least four times and may repeat as many as six times, with only minor differences in the repeat unit. Further analysis confirmed that the *hagA* gene has four large contiguous direct repeats totalling 5,404 bp in length, each ranging from 1,318 to 1,368 bp in length.

Specifically, these approximately 1.3 kb repeat fragments, collectively referred to hereinafter as *HAreps*, are (referring to bp number of *EcoRV* fragment): *HAreps*1, bp 1862-3211 (SEQ ID NO. 15); *HAreps*2, bp 3212-4579 (SEQ ID NO. 17); *HAreps*3, bp 4580-5947 (SEQ ID NO. 19); and *HAreps*4, bp 5948-7265 (SEQ ID NO. 21). The deduced amino acid sequences for the nucleotide repeat fragments *HAreps*1, *HAreps*2, *HAreps*3, and *HAreps*4 are shown as SEQ ID NOS. 16, 18, 20, and 22, respectively. This repeat unit has been shown to have hemagglutinin activity. The results of the hemagglutinin assay for strains having varying numbers of *HAreps* repeat units are shown in Table 5, below.

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Table 5. Hemagglutinin titer

Strain	No. of <i>HAreps</i>	A ₆₆₀	HA titer
381 (wild-type strain)	>4	0.13	1/128
<i>pNH9</i>	1	3	1/8
<i>pNH1</i>	2	0.85	1/64
<i>E. coli</i>	0		

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When compared with that of *hagA*, several reported protease genes were found to contain at least one copy of the *HAreps* sequence. For example, *prtH*, a gene encoding a C3 protease cloned from strain W83, shares a region of 271 amino acids with 95.6% homology to *hagA*. *Rgp-1*, the arginine-specific cysteine protease/hemagglutinin gene cloned from strain H66, contains a 522-amino acid region with 93.1% homology, as well as *prtR* cloned from strain W50. *Agp*, cloned from strain 381 by Okamoto *et al.*, and *prpR*, cloned by Curtis *et al.*, which are identical genes to *rgp-1* isolated from different strains, each contain one *HAreps* sequence of *hagA*. An additional gene, *agp*, which is missing a 713-amino acid internal portion of *rgp-1*, also contains one *HAreps* sequence. In addition, *prtP*, a cysteine protease/hemagglutinin gene cloned from strain W12 and described herein, has an 849-amino acid C-terminal region which shares 92.2% homology to *hagA*, with the last 253 amino acids (almost half of the length of the *prtP* gene) absolutely identical. *Tla*, another protease gene cloned from strain W50 by Curtis *et al.*, has a 789-amino acid C-terminal region with 95.2% homology to *hagA*, with the last 171 amino acids completely identical. This 171-amino acid region constitutes almost three-fourths of the length of the *Tla* gene. In addition, *hagD*, a fourth hemagglutinin gene cloned from strain 381, described hereinbelow, has a 523-amino acid region with 92.7% homology, as well as the 3' 72-amino acid with 98.6% identity to *hagA*. *HagE*, an additional hemagglutinin gene cloned from strain 381, also described hereinbelow, contains a 518-

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amino acid region with 92.3% homology to *hagA*. Without exception, these high homology regions of each of these genes are within or extend from the repeat region of *hagA*. The *hagA* is a central member of a multigene family which share the *HAre*p sequence.

In addition, each of these genes contains a common 72-amino acid C-terminus with *hagA*
5 (81.9 to 100% homology), except for *prtH*, in which this region is located in the middle of the gene.

A search through the National Center for Biotechnology Information Database using the GENINFO Experimental Blast Network Service revealed no significant homology of *hagA* to any other sequences in the databases except for the *Mycoplasma gallisepticum* hemagglutinin genes
10 (pMGA) and the circumsporozoite protein genes of *Plasmodium falciparum*. These genes were found to have homology to *hagA* in very short regions (9 of 13 amino acids for the circumsporozoite protein of *P. falciparum* and 11 of 14 amino acids for pMGA of *M. gallisepticum*).

To ensure that the complete *hagA* gene sequence was isolated from clone 2, chromosome DNA samples were digested by restriction enzymes which did not cut the original cloned fragment
15 clone 2, including *AccI*, *AseI*, (Biolabs) *VspI* (the isoschizomer from Promega), *BclI*, *BglII*, *BstXI*, *DraI* (BRL), *EcoRV*, *NruI* (Stratagene), *PstI*, *PvuII*, *SalI*, *SphI*, *SspI*, *SstI* (Sigma), *SnaI*, and *XhoI*. The digested fragments were transferred to positive-charged nylon membranes (Boehringer Mannheim Biochemicals, Indianapolis, IN) by capillary transfer method. The whole ST2 fragment was labeled and detected by nonradioactive Genius Kit (Boehringer Mannheim Biochemicals).
20 Alternatively, a region of the first 394 bp of clone 2, which is distant from the repeat sequence region, was labeled using the nonradioactive DIG DNA Labeling and Detection Kit (Boehringer Mannheim) and used as a probe to detect the bound DNA fragments on the nylon membrane. The results were made visible on X-Ray films by Lumi-phos 530 system (Boehringer Mannheim Biochemicals).

25 Inverse polymerase chain reaction (IPCR) was employed to determine the complete sequence of a gene, and was used to obtain the flanking 5' and 3' sequences and thus the entire nucleotide sequence of the *hagA* gene. To carry out the IPCR procedure, two 18-mer oligo primers, negative primer at position nt 224 and positive primer at position nt 2032, were chosen and synthesized at University of Florida DNA Synthesis Core Lab. In addition, a negative primer at 405 nucleotide (t)
30 upstream of the 5' end of the ST 2 fragment (GGC AAA CCA AAA AGA TTC, SEQ ID NO. 23) and a positive primer at 529 nt 3' of the ST 2 fragment (TTC TTC CAA CGA CTA CAC, SEQ ID NO. 24) were selected and synthesized at the University of Florida DNA Synthesis Core Facility.

The total *AseI* (*VspI*) digested fragments and the 3-7 kb fragments extracted from agarose gel were self-ligated at a DNA concentration of 1-10 ng/μl with 1 U of T4DNA ligase (Promega)

per 50 µl reaction mixture for 16 hours at 16°C, respectively. Then, the ligation mixture was heated for 15 minutes at 65° and extracted with phenol/chloroform, chloroform, precipitated with ethanol and resuspended in sterilized distilled water. IPCR reactions were performed in 2 steps: first, the self-ligated DNA sample in buffer was heated for 30 minutes at 94°C; then, Taq polymerase (Promega) was added and cycled using a PTC-100 Programmable Thermal Controller (MJ Research, Inc., Watertown, MA). We used 35 cycles of denaturation at 94°C for 1 minute, primer annealing at 52°C for 1 minute, and extension at 72°C for about 5 minutes.

The amplified mixture was extracted with phenol/chloroform, chloroform and electrophoresed at 1% low melting agarose gel. The excised fragment was then treated with agarase (Boehringer Mannheim Biochemicals). The DNA samples treated with agarase are purified enough for direct sequencing. After analysis of direct sequencing data, the amplified IPCR fragment was cut by *HindIII* and *KpnI* and cloned into pBluescript II SK and transformed in *E. coli* JM 109. Several subclones were constructed and one oligo primer was also synthesized to complete the sequencing.

Sequencing of the *hagA* gene was carried out at the University of Florida DNA Sequencing Core lab using the Taq Dye Primer and Taq Dyedexy Terminator Cycle Sequencing Protocol developed by ABI (Applied Biosystems, Inc., Foster City, CA) with fluorescent labeled primer(s) and labeled dideoxy nucleotides, respectively. The labeled extension were analyzed on an ABI 373 DNA Sequencer. Sequence data were analyzed by the Sequence Analysis Software Package of the University of Wisconsin.

Southern blot analysis results indicated that *AseI* restriction of genomic DNA produced a single 6.9 kb fragment which hybridized to the probe used. Under the conditions used, as described, a 5,963 bp fragment was successfully amplified via IPCR which, when sequenced, was found to include an additional 2,997 bp sequence 3' to the ST 2 fragment. The start codon was found to be located 720 bp upstream of the 5' end of the ST 2 fragment. In order to obtain the 3' end of this gene, a *BamHI* gene bank was constructed from which an 8,818 bp cloned fragment containing an additional 3,362 bp downstream DNA was obtained. Sequencing this downstream region revealed that the stop codon was located 1,017 bp downstream of the 3' end of the 6.9 kb *AseI* fragment.

The complete ORF of *hagA* beginning at base No. 365 and ending at base No. 8251 is calculated to encode a 2628-amino acid protein with a molecular weight of 283.3 kD. Analysis of the sequence revealed potential -10, -35 consensus sequences located at bases 168 and 143, respectively. However, no *E. coli*-like ribosome binding site was found upstream of the start codon except for AGG at the -4 to -2 position. Two potential stemloop structures, forming 14 and 9 bp-long inverted repeats were identified 51 and 101 bp downstream of the stop codon, respectively.

Residues No. 5-21 are consistent with a typical, hydrophobic leader or signal sequence according to the Chou-Fasman Prediction. In addition, Chou-Fasman rules predict the beginning amino acids of *HAreps* to be very antigenic and hydrophilic. The amino acid sequence which begins each of the *HAreps*, is very similar to a region of *M. gallisepticum* hemagglutinin genes. The common repeating amino acid sequence (Pro-Asn) among *P. gingivalis* and *M. gallisepticum* hemagglutinin genes listed above indicates that this region is involved in erythrocyte binding.

The repeat region was found to begin immediately after the first *KpnI* site at base No. 1862 and to end at base No. 7265, making the entire repeat region 5,404 bp in length without a single gap. The first repeat unit (*HAreps* 1) is 1,350 bp and has 99.5% identity to the second repeat unit. The repeat units *HAreps* 2 and *HAreps* 3 are 1,368 bp in length and are 99.9% identical to each other. The fourth repeat unit (*HAreps* 4) is 1,318 bp in length and has 98.6% identity to *HAreps* 2 and *HAreps* 3, respectively. As shown in SEQ ID NO. 16, the beginning amino acid sequence of the *HAreps* 1 is "Pro Asn Pro Asn Pro Gly Thr Thr Thr ..." while that of the other three is "Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn Pro Gly Thr Thr Thr ..." (see SEQ ID NOS. 18, 20, and 22). Thus, *HAreps* 2-4 at the very beginning contain six amino acids more than *HAreps* 1. This difference is due to *HAreps* 1 containing two fewer repeats of the Pro-Asn sequence since the Gly-Thr is present before the sequence of "Pro Asn Pro Asn Pro Gly Thr Thr Thr ..." in *HAreps* 1.

Another distinguishing characteristic of the *hagA* multigene family is the presence of a 72-amino acid sequence normally at the extreme carboxy terminus of the proteins. This region is hydrophobic according to the Chou-Fasman Prediction and can serve to anchor the proteins in the outer membrane or serve in some other common recognition function.

The hemagglutinin (HA) encoded by the *hagA* gene can have the characteristics of a cysteine protease, a trypsin-like protease, and a hemagglutinin. Hemagglutinins of *Porphyromonas gingivalis* can be involved in virulence. The HAs of *P. gingivalis* are nonfimbrial adhesins, since biochemical studies have shown that the purified fimbriin subunit of *P. gingivalis* failed to agglutinate red blood cells or to inhibit hemagglutination by *P. gingivalis*, and immunological studies have shown that monospecific antibody against the hemagglutinin did not bind strongly to the fibrillar structures of *P. gingivalis*.

It has been previously suggested that protease and hemagglutination activities of *P. gingivalis* are related. One study reported that mutant strains of *P. gingivalis* deficient in trypsin-like protease activity had markedly reduced hemagglutination activity. Others have reported that a 44 kD purified outer membrane hemagglutinin has been further characterized as a cysteine protease. The DNA sequence of *hagA* was compared with the DNA sequence of an approximately 4.5 kb fragment of genomic DNA from the λ FBP1 clone made from the of *P. gingivalis* W12 strain. The

gene from the λ FBP1 clone was isolated and named *priP* (see section F of this Example, below). The *priP* gene encodes protein(s) reactive with antibody that inhibits a cysteine protease of *P. gingivalis* W12, and that binds a fibrinogen. The nucleotide sequences of *hagA* and *priP* were compared, and were found to contain internal regions approximately 2 kb in size that share a high degree of sequence similarity. The *hagA* gene contains three regions that share greater than 90% sequence identity with *priP*. These regions include a 217 bp sequence in which there is 90% identity, and a 884 bp sequence in which there is 94% identity and a 500 bp sequence in which there is 97% identity. These findings raise the possibility of relatedness between fibrinogen binding protein and a hemagglutinin of *P. gingivalis*.

B. Characterization of *hagB* gene and gene product. The gene encoding a hemagglutinin *hagB* was obtained for sequencing from *P. gingivalis* on a 2.0 kb *HindIII* *Bam*HI fragment and 2.4 kb *Bam*HI-*Eco*RI fragment cloned into pUC9 and transformed into *E. coli* JM109. These fragments were subcloned into the M13 bacteriophage vectors for sequencing (Yannish-Peron, C., J. Vicra, J. Messing [1985] "Improved M13 phage cloning vectors and host strains: Nucleotide sequences of M13mp18 and pUC9 vectors," *Gene* 33:103-119). The entire lengths of these fragments were sequenced utilizing the universal priming site of M13 and by synthesizing oligonucleotide primers for the remaining regions of the fragments. The sequencing of the 1.7 kb *Kpn*I-*Pst*I fragment and the DNA adjacent to the *Bam*HI site ensured that the 2.0 kb and 2.4 kb fragments were contiguous. *E. coli* JM109 was used as the host strain for transfection with M13 and grown in 2x YT broth. Recombinant phages were detected by using soft agar (0.75%) overlays of 2x YT broth base supplemented with 0.33 mM isopropyl-beta-D-thiogalactopyranoside (IPTG) and 0.02% 5-bromo-4-chloro-3-indolyl-3-galactoside (X-GAL).

Restriction enzymes, T4 DNA ligase, and M13 17-mer primer were purchased from either Bethesda Research Laboratories (Gaithersburg, MD) or Fischer Scientific Co., St. Louis, MO) and were used in accordance with the specifications of the manufacturers. Other oligonucleotide primers were synthesized by the Molecular Biology Resource Facility (Oklahoma City, OK). Sequencing reagents were from the T7 Sequencing Kit of Pharmacia (Piscataway, NJ) or the Sequenase DNA sequencing kit of U.S. Biochemical Corp. (Cleveland, OH). The [α - 35 S]dATP was purchased from DuPont, NEN Research Products (Boston, MA). IPTG and X-GAL were purchased from Sigma Chemical Co. (St. Louis, MO).

DNA sequencing was performed by using the dideoxy chain-termination method (Sanger, F., S. Nicklen, A.R. Coulson [1977] "DNA sequencing with chain terminating inhibitors," *Proc. Natl. Acad. Sci. USA* 74:5463-5467). Different portions of each fragment were sequenced from synthesized oligonucleotide primers. The DNA sequence of the gene was determined for both

strands and was analyzed by the James M. Pustell DNA and protein sequencing program (International Biotechnologies, Inc., New Haven, CT). The nucleotide sequence of the *hagB* hemagglutinin gene is 1053 nucleotides in length as shown in SEQ ID NO. 3. The mol.% G+C content is 59.9%. The reading frame of the hemagglutinin gene was defined by a putative ribosome binding site and promoters upstream of the ATG start codon and potential stem-loop structures downstream of the stop codon. Beginning 181 to 239 bases upstream of the two potential promoters was a region of direct repeats. A sequence of 41 nucleotides was repeated four times contiguously with only minor differences. Open reading frames were also identified on the opposite strands both upstream and downstream of the hemagglutinin gene.

The amino acid sequence of the hemagglutinin was derived from the nucleotide sequence and determined to be 350 residues in length. The derived protein of $M_r=39,375$ was basic with an isoelectric point of 8.98 and hydrophilic. A potential signal peptide is evident. Cleavage is most probable after amino acids 32-36, though none of these sites conforms ideally to the -3,-1 rules of von Heijne. The derived amino acid sequence encoded by the *hagB* gene is shown in SEQ ID NO.

Comparison of the nucleotide and derived amino acid sequences with the gene and protein bank libraries did not uncover any significant homology between the hemagglutinin and previously determined sequences.

Upstream from the hemagglutinin reading frame were two potential promoters which in turn were preceded by a series of direct repeats. The function of the direct repeats is not known but it would be reasonable to hypothesize that they have a role in gene expression.

The codon usage for the hemagglutinin was examined and found to follow the pattern for a gene with low level expression, though this pattern was broken in a few instances. In general, the pattern for low expression consists of a low U/C ratio in the third base position of the codon for some amino acids, but a high U/C ratio in the third position for other amino acids. Perhaps due to the high %G+C content of the hemagglutinin gene a low U/C ratio existed for most amino acids. Overall, however, the codon usage followed the pattern for low expression more often than that for high expression. The usage of some codons which specify rare tRNA species in *E. coli* may also be evidence of a lower level of expression of the hemagglutinin gene. Alternatively, the same tRNA species may not be rate limiting in *P. gingivalis* but could explain the difficulty in expressing the cloned product in *E. coli*.

C. Characterization of the *hagC* gene and gene product. A third hemagglutinin gene, designated *hagC* was isolated from *Porphyromonas gingivalis* 381. The nucleotide sequence of the

hagC gene is shown in SEQ ID NO. 5 and has a 1050 bp coding region. The derived amino acid sequence is shown in SEQ ID NO. 6.

The *hagC* gene was isolated in a similar manner as the *hagB* gene. Briefly, isolated *P. gingivalis* 381 chromosomal DNA was digested with *Hind*III and electrophoresed through a 0.8% agarose gel in Tris-acetate buffer. A band of agarose containing the fragments ranging from 4 to 20 kb was cut out of the gel and the DNA extracted using a phenol freeze/thaw procedure. The DNA was ligated to the dephosphorylated *Hind*III restricted pUC18 plasmid (Pharmacia LKB Biotechnology, Piscataway, NJ) using the T4 DNA ligase (Promega Corp.) overnight at 16°C. The recombinant plasmids were transformed into *E. coli* DH5 α (BRL) and plated on LB plates supplemented with ampicillin, IPTG and X-GAL. Colonies were picked on duplicate plates and grown aerobically at 37°C overnight. The clones from one of the duplicated plants were transferred to positively charged nylon membranes (BM Corp.) and lysed according to the procedure described by Sambrook *et al.* The membranes were then left to dry for 30 minutes and baked at 120°C for 30 minutes. The hybridization was carried out as described above; however, a 960 bp *Bam*HI-*Pst*I DNA fragment from *hagB* gene was used as a probe.

Recombinant plasmid DNA was prepared using the alkaline lysis method, modified as described. The cells were grown in LB broth supplemented with 50 μ g/ml ampicillin. The closed circular DNA was purified by equilibrium centrifugation in a continuous CsCl-ethidium bromide gradient. DNA further destined for sequence was additionally submitted to precipitation with polyethylene glycol.

Double stranded DNA sequencing was performed by the University of Florida Interdisciplinary Center for Biotechnology Research DNA Sequencing Core laboratory. Sequencing was accomplished by employing the Taq Dye Primer and Taq Dye Terminator cycle sequencing protocols (Applied Biosystems, Inc., Foster City, CA) using the fluorescent primers and dideoxynucleotides, respectively. The labeled extension products were analyzed on an ABI373a DNA sequencer (Applied Biosystems, Inc.). The sequence was obtained for both strands of DNA using the appropriate subclones or synthetic oligonucleotides synthesized by the University of Florida DNA Synthesis Core Facility. the sequencing strategy was designed to sequence overlapping sites used in DNA subcloning. The sequence was analyzed with the Genetic Computer Group Sequence analysis software.

The 1851 bp *Hind*III-*Sst*II DNA fragment comprising the *hagC* gene revealed an open reading frame (ORF) of 350 amino acids corresponding to a 39.3 kD protein with an isoelectric point of 8.36. The ATG start site, located at position 374 of the DNA, is preceded by putative -10 (³³⁹TATTAT³⁴⁴) and -35 (³¹⁴TTGCTG sequences which differ from the *E. coli* consensus promoter

sequences TATAAT and TTGACA, by one and three nucleotides respectively. However, no match to consensus Shine-Dalgarno sequence could be found upstream the ATG codon. A nearly perfect dyad symmetry of 18 nucleotides can be noticed at the end of the *hagC* ORF and may represent a potential stem-loop structure used in transcription-termination.

5 A comparison between the *hagB* and *hagC* nucleotide sequences revealed that their ORFs are 99% homologous, but their upstream and downstream regions are only 39.5 and 34.6% homologous, respectively. It is worth noting that both genes encode a 350-amino acid protein which are 98.6% homologous. The Hag B protein exhibits a deduced MW of 39.4 kD and pI of 8.98. The *hagB* gene possesses two sets of -10 and -35 sequences which are similar to the consensus
10 sequences found in *E. coli*. Contrary to *hagC* however, a ribosome-binding site can be noted upstream the ATG initiation codon in position 363. Furthermore, four repeats of 42 bp each that are found in the promoter region of *hagB* are missing from the *hagC* gene. A potential transcription-termination stem-loop made by a nearly perfect 17 nucleotide long dyad symmetry can also be noted at the end of the *hagB* gene. No nucleotide sequence or protein exhibiting significant homology to
15 the *hagC* gene or protein was found using the data bases GenBank, EMBL, or NBRF.

D. Characterization of the *hagD* gene and gene product. A fourth hemagglutinin gene, designated as *hagD*, was isolated from *P. gingivalis* 381 using standard procedures as described. The original nucleotide sequence comprising the *hagD* gene is shown in SEQ ID NO. 7. The *hagD* ORF as originally determined codes for a 1087 amino acid, 117 kD protein with a pI of 4.5. The
20 derived amino acid sequence encoded by the original *hagD* gene is shown in SEQ ID NO. 8. The nucleotide sequence for the entire *hagD* gene is shown as SEQ ID NO. 25. Two open reading frames were identified within the *hagD* nucleotide sequence. The first open reading frame, bases 696-1790, encodes a polypeptide shown as SEQ ID NO. 26. This polypeptide can have activity as a protease. The second open reading frame, bases 1790-5866, encodes a polypeptide shown as SEQ ID NO. 27.
25 The second encoded polypeptide has activity as a hemagglutinin.

 The *P. gingivalis* 381 cells were grown at 37°C in Todd-Hewitt broth (THB) supplemented with 5 µg/ml hemin and 1 µg/ml menadione in an atmosphere of 10% H₂-5% CO₂-85% N₂. *Hind*III-restricted genomic DNA was then electrophoresed through TAE agarose gel (9%). The DNA was transferred to a nylon membrane by the capillary alkaline transfer method using 0.4 M NaOH-0.6
30 M NaCl and labeled using the nonradioactive DNA labeling and detection kit (Genius, Boehringer Mannheim). The membrane was prehybridized for 2 hours at 42°C in 5X SSC (0.75 M NaCl, 0.085 M sodium citrate (pH 7.0); blocking agent 0.5% (w/v); N-lauroylsarcosine (Na-salt), 0.1% (w/v); sodium dodecyl sulfate (SDS), 0.02% (w/v); formamide 50% (v/v)).

The *EcoRI-PvuII* DNA fragment from *hagA* was randomly primed by incorporation of digoxigenin-labeled dUTP. Hybridization was carried out overnight at 42°C. The membrane was washed twice with each of the following solutions: 2X SSC-0.1% (w/v) SDS at room temperature for 5 minutes, and 0.1X SSC-0.1% (w/v) SDS at 68°C for 15 minutes. Detection was carried out using "LUMI-PHOS" 530 (Boehringer Mannheim), the enhancer for chemiluminescent detection of alkaline phosphatase, according to the manufacturer, and autoradiographed.

A genomic bank was created using *HindIII*-digested chromosomal DNA from *P. gingivalis* 381, as described above for *hagC*. Fragments ranging from 4.8 to 6.4 kb were cut out and the DNA was recovered using the phenol freeze/thaw procedure. The DNA was then ligated to the dephosphorylated *HindIII* restricted pUC18 (Pharmacia) using T4 DNA ligase overnight at 16°C.

Recombinant plasmids were transformed into *E. coli* DH5 α (BRL) and plated on Luria-Bertani (LB)(10 g/l Bacto®Tryptone, 5 g/l yeast extract, 5 g/l NaCl, 15 g/l agar) plates supplemented with 50 μ g/ml ampicillin. Colonies were picked, transferred to nylon membranes, and subjected to lysis in 10% (w/v) SDS, 3 minutes; 0.5 N NaOH-1.5 M NaCl, 5 minutes; 1.5 M NaCl-0.5 M Tris-Cl (pH 7.4), 5 minutes; and 2X SSC, 5 minutes. The membranes were then left to dry for 30 minutes and baked at 120°C for 30 minutes. Prior to hybridization the membranes were washed in: 5X SSC, 0.5% SDS, 1 mM EDTA (pH 8.0) for 30 minutes at 50°C. Hybridization was then carried out as described above using a 1,228 bp *HindIII-SmaI hagA* DNA fragment as a probe.

Plasmid DNA was isolated and restriction mapping, was carried out according to procedures described.

Double-stranded DNA sequencing was performed by the University of Florida ICBR DNA Sequencing Core Laboratory. Sequencing was accomplished by employing the Taq Dye Primer and Taq Dye Terminator cycle sequencing protocols using the fluorescent primers and dideoxy nucleotides, respectively. The entire sequence was obtained for both strands of DNA using the appropriate subclones or synthetic oligonucleotides synthesized by the University of Florida DNA Synthesis Core Facility. The sequencing strategy was designed to sequence overlapping sites used in DNA subcloning.

The complete sequence was determined using the Genetic Computer Group Sequence analysis software and the inverse polymerase chain reaction (IPCR) method. For the IPCR procedure, 50-500 ng of *P. gingivalis* genomic DNA restricted with *Bam*HI was circularized and self-ligated with T4 DNA ligase overnight at 16°C. The circularized genomic DNA was amplified by IPCR in a mixture containing: 160 mM each dNTPs, 1.5 mM MgCl₂, 1X Buffer [1X=50 mM KCl, 10 mM Tris-HCl (pH 8.3)], 4x10⁻⁴ mM of the primers APF 147 (5'-GGAATGGGAGATGGAAC-3') (SEQ ID NO. 11) and APF 148 (5'-

GTAACCCGTATTGTCTCC-3') (SEQ ID NO. 12) and 5 U Taq I. The IPCR amplification was accomplished with the "PTC-100" Programmable Thermal Controller (MJ Research, Inc.) for 5 linked files as follows: (1) 30 minutes at 94°C for 1 cycle after which the Taq I was added; (2) 1 minute at 94°C; (3) 1 minute at 52°C; (4) 5 minutes at 72°C, repeat steps 2,3, and 4, 34 more times; (5) 10 minutes at 72°C. The amplicon was gel purified and the DNA was extracted using agarase. The purified amplicon was sent to be sequenced using APF 147 (SEQ ID NO. 11) as the primer.

The recombinant plasmid comprising the *hagD* gene in *E. coli* expressed four proteins which were subjected to SDS-PAGE electrophoresis under denaturing conditions a doublet corresponding to proteins with Mr of 90 and 85.8 kD, as well as an 80 kD and a 20 kD protein. Based on the intensity of the bands, the 80 kD protein appeared to be the most strongly expressed. A comparison between *hagD* and *hagA* amino acid sequences revealed that they possess an overall homology of 73.8% composed of a central region with 90% homology flanked by regions sharing less than 60% homology. Hag D was also found to possess high homology (89.5%) to the *priP* gene product isolated from the strain *P. gingivalis* W12. The N-terminus region of these two proteins was found to be more homologous (90%) than the C-terminus (72%). It is therefore possible that *hagD* and *priP* gene products represent different alleles of the same gene which evolved, from a common ancestral strain and diverged. Both *hagA* and *hagD* transcripts, as determined by reverse PCR analysis, were detectable only in hemin-replete conditions as previously reported for *hagC*. These results show that *hagA*, *hagC*, and *hagD* might be coordinately regulated by hemin while *hagB* is differentially expressed.

E. Characterization of the *hagE* gene and gene product. Using a repeated sequence of *hagA* as a probe, an additional fragment approximately 2.6 kb in length was detected in *P. gingivalis* 381 genomic DNA by Southern analysis. In order to clone this fragment, a genebank was constructed from *P. gingivalis* strain 381 genomic DNA and screened by *in situ* hybridization with the probe. A total of 59 positive colonies were identified. Restriction enzyme digestion of mini-preparations of plasmid DNA from 8 positive colonies revealed that 7 of them contained the expected fragment. Hemagglutination assay demonstrated that the cloned fragment in one orientation conferred a high level of hemagglutination activity on the *E. coli* host strain but no activity when the fragment was in the opposite orientation. Sequencing data confirmed that the 5' sequence of the clone is unrelated to that of *hagA* while the 3' sequence of 600 bp has high homology to *hagA*. This homology occurs in the area of the 1.3 kb repeat in *hagA*. This discovery of yet another gene, designated *hagE*, with areas of homology to *hagA*, may indicate that these genes represent a multi-gene family with similar

functions and perhaps identical active sites. It is likely that such duplication indicates an essential or important function to the bacterial species and its interaction with the host.

By constructing a gene library, an 8.64 kb fragment was obtained which, when sequenced, was found to contain the complete open reading frame (ORF) of *hagE*. This ORF is 5,064 bp in length and encodes a 1,687 amino acid, 183.7 kD protein. The nucleotide and amino acid sequences for *hagE* are shown as SEQ ID NOS. 28 and 29, respectively. Two other ORFs were found in *hagE* between nucleotides 6580-7551 and 7716-8640, respectively. When comparing the sequence of *hagE* with that of *prtH*, which encodes a C3 protease from strain W83, it was found that the whole 3,658 bp cloned fragment of *prtH* was within the clone comprising *hagE*. The *hagE* fragment contains an additional 3,761 bp 5' and 1,327 bp 3' of the *prtH* fragment. The homology of the common sequence is 98%. However, there are also 16 gaps in comparing the two sequences, including one base deletion, 13 one-base, and 2 two-base additions in *prtH*. This is likely due to strain differences. However, a sequence of an additional protease gene (*rpg-I*) reported from another strain (HG66) showed only 2 gaps in this region and maintained the ORF in relation to *hagE*. Most interestingly, translation analysis of our cloned fragment showed there is no *prtH*-like ORF present. Therefore, *prtH* is likely not present in *P. gingivalis* strain 381. In addition, two additional ORFs directly downstream of *hagE* were identified within the cloned fragment. The sequencing of *hagE* has revealed it to be a member of the *HagA* multi-gene family.

F. Characterization of the *prtP* gene and gene product. A gene and polypeptide having homologous regions to those of the *hagA*, *hagB*, *hagC*, *hagD*, and *hagE* genes and gene products were isolated from *Porphyromonas gingivalis* W12. The *P. gingivalis* DNA insert in λ FBP1 was 4.5 kb (pHW2) and was subcloned for sequencing. It contained a large open reading frame, which encodes approximately the carboxy-terminal two-thirds of the cysteine proteinase, porphypain. The complete gene encoding porphypain was obtained using PCR and IPCR technology. The gene, which has a nucleotide sequence as shown in SEQ ID NO. 9, is designated *prtP*. The deduced amino acid sequence of the *prtP* gene is shown in SEQ ID NO. 10.

Four repeated amino acid sequences and more than five Pro-Asn tandem repeats were identified in the carboxy-terminal three-fifths of the gene. Repeat 1 includes amino acid segments 688-708 and 946-967; repeat 2 includes three amino acid segments 887-952, 1341-1405, and 1607-1650; repeat three includes amino acids 985-1006 and 1430-1451; and repeat 4 includes amino acids 1041-(1100) and 1488-(1547). These repeats can be functionally or structurally important. For example, a Pro-X motif in the TonB protein has been implicated in crossing the periplasmic space. Based on Southern blot analyses, Repeat 2 was present in at least 20 copies in each of the seven *P. gingivalis* genomes examined. The pattern of bands observed in these analyses was very similar for

strains W50 and W83, but not identical; these strains have been previously indistinguishable when analyzed by multilocus enzyme electrophoresis, DNA fingerprinting, and arbitrarily primed PCR. Therefore, the repeats can be useful for distinguishing *P. gingivalis* strains. Strains ATCC 33277 and 381 showed an identical banding pattern in our analysis, which supports previous analyses characterizing the relatedness of the strains and the suggestion that strain ATCC 33277 is actually a derivative of strain 381.

Several other *P. gingivalis* genes with homology to *prtP* have been described. Most of *hagA*, which encodes a hemagglutinin identified originally in strain 381 was highly homologous to the C-terminal portion of *prtP*, including four-and-a-half copies of a large DNA segment encompassing the *prtP* Repeat 2 sequence. Our data were consistent with the presence of *hagA* in the seven strains examined. Certain evidence suggests that an extracellular form of PrtP participates in hemagglutination, indicative of the function of the large region the proteins have in common. Five proteinase genes previously identified in *P. gingivalis* were also found to be partially homologous to *prtP*: *rgp-1*, *prpR1*, *prtR*, *prtH*, and *agp*. Each of these genes is thought to encode a proteinase with Arg-X specificity, but not Lys-X specificity, and none of them had homology to the N-terminal portion of PrtP. The subject proteinases from the subject strain W12 have been demonstrated to degrade fibrinogen and fibronectin and hydrolyze both N-*p*-tosyl-Gly-Pro-Lys-*p*-nitroanilide and N-*p*-tosyl-Gly-Pro-Arg-*p*-nitroanilide.

Genomic DNA from *Porphyromonas gingivalis* W12 was isolated using standard procedures, as described herein and was purified and disrupted by shearing. *EcoRI* linkers were ligated to the ends of *P. gingivalis* DNA fragments of appropriate sizes, and the fragments were cloned into the λ gt11 vector. The λ gt11 library was screened using polyclonal antibodies raised against a 120-kD cysteine proteinase (porphypain), purified from *P. gingivalis* W12. Several clones were isolated that reacted strongly with the anti-proteinase antibody. One of the clones, λ FBP1, reacted strongly with the antibody, and contained a protein which bound fibrinogen.

The gene *prtP* has an open reading frame extending from bases 696 to 5894 and encodes a unique protein of 1732 amino acids, including a putative signal sequence for protein secretion. The predicted molecular mass for the mature protein was 186 kD, which is close to the observed molecular mass of 180 kD. There was one copy of *prtP* in the genomes of seven *P. gingivalis* strains examined (ATCC 33277, 381, W50, W83, W12, HG66, and ATCC 53977). The gene is located 5' to a region with a high degree of homology to the insertion element IS1126 in *P. gingivalis* strain W12. The PrtP protein had regions of high homology to Hag A, a hemagglutinin of *P. gingivalis*, and to several purported proteinases of *P. gingivalis* that have Arg-X specificity. A detailed comparison of genes encoding the latter and *cpgR* indicates that *rgp-1*, *prpR1*, *prtR*, *agp*,

cpgR, and possibly *prtH* can be derived from identical genetic loci. Although an *rgp-1*-like locus was detected in seven *P. gingivalis* strains by Southern blot analyses, *agp* and *cpgR* were not detected, not even in the strains from which they were originally isolated. In addition, at least 20 copies of a repeat region common to PrtP, the Rgp-1-like proteins, and Hag A were observed in each of the seven genomes examined. The repeat region hybridization patterns for strains W83 and W50 were very similar, and they were identical for strains 381 and ATCC 33277, providing further evidence that these strains are closely related genetically.

P. gingivalis organisms produce a number of proteolytic enzymes which are found both extracellularly and associated with the bacterial cell surface. Most of these *P. gingivalis* enzymes have been referred to previously as "trypsin-like," based on their preferential hydrolysis of proteins and peptides on the carboxyl side of basic amino acid residues. However, the designation is inappropriate because all of the enzymes that have been recently characterized indicate they are cysteine proteinases.

The large, cell surface-associated cysteine proteinase (porphypain; PrtP) from *P. gingivalis* W12 can hydrolyze synthetic peptide substrates with either arginine or lysine residues in the P₁ position. Hydrolysis of both Arg-X substrates and Lys-X substrates is activated by reducing agents (Cysteine >> β -mercaptoethanol = DTT), and derivatives of glycine stimulate both activities. Both activities are inhibited by EDTA; however, hydrolysis of Arg-X substrates is inhibited by leupeptin and preferentially by Tyr-Pro-Arg chloromethyl ketone (YPRCK) over TLCK, and hydrolysis of Lys-X substrates is unaffected by leupeptin and preferentially inhibited by TLCK over YPRCK, indicating the presence of two types of active sites. The porphypain of the subject invention can contain two separate enzymes or a single enzyme which has one active site with two different conformations—one which accepts lysine in P₁, and the other which accepts arginine in P₁.

Example 14 – Construction of DNA Probes

DNA-DNA hybridization assays (DNA probes) are based on the fact that single-stranded DNA will re-anneal only with a complementary strand of DNA whose sequence is homologous. More recently, DNA probes have been used as a means of detecting various infectious agents and some are now used routinely in clinical microbiology laboratories. The identification of DNA sequences of oral *Porphyromonas* sp. make it possible to create DNA probes for the identification of these species. Therefore, one application of the identification and isolation of genomic sequences which encode bacterial antigens is the use of the DNA fragments as DNA probes. In the current case, these probes may comprise the *Porphyromonas* clones identified herein, or fragments of these

clones. Also, the DNA sequence shown in SEQ ID NOS. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 28, or fragments of those sequences, can be used to construct suitable probes.

Each recombinant plasmid is isolated and digested with whichever restriction enzyme was used to generate that particular genomic library. The digested plasmid DNA is then separated electrophoretically on an agarose gel as described earlier. The *Porphyromonas* DNA band containing the fragment is cut out of the gel and the DNA fragment is recovered by electro-elution employing centrifugal filtration of DNA fragments through a Durapore (Millipore) membrane inside a conical tip. This rapid and simple method recovers 70% of the DNA in a highly pure state.

The conical tip is assembled as follows: the conical portion of a 1.5 ml Eppendorf tube is cut off and a hole pierced in the bottom with a thin wire. A 4.5 cm² piece of Durapore (Millipore) membrane is wetted (d. H₂O) on a piece of parafilm, the filter square is then formed around a blunt-ended glass rod, and the filter is placed inside the conical bottom (cone). Excess filter is cut away, the filter tip is placed inside a 1.5 ml Eppendorf tube, and the filter is prewetted with 200 µl of elution buffer (0.1% SDS + 50 mM Tris-HCl, pH 7.5). The gel slice is then transferred to the prepared conical tip. After centrifugation of the DNA preparation in a microcentrifuge (Eppendorf) for 10 minutes, the filtered aqueous phase containing the DNA is precipitated by the addition of 5 M NaCl (to 1 M) and two volumes of ethanol. After ethanol precipitation, the DNA fragment(s) is labeled non-radioactively, using a photo-activatable biotin tag as described by the supplier (Clontech Laboratories, Inc.).

For biotin labelling, the DNA fragment preparation is adjusted to a concentration of 1 mg/ml (TE) and is mixed with photo-activatable biotin (PAB) at a ratio of 1:3 (DNA:PAB) in a 1.5 ml Eppendorf tube. The tube is placed in an ice bath 10 cm below a 275 W (GE RSM) sunlamp and the DNA + PAB is irradiated for 15 minutes. The DNA solution is then mixed with an equal volume of 0.1 M Tris-Cl (pH 9.0) and the volume adjusted to ≥ 100 µl with H₂O. The unincorporated PAB is extracted from the DNA by the addition of an equal volume of 2-butanol, vortexing, centrifuging briefly, and withdrawing the lower aqueous phase with a Pipetman. The extraction can be repeated to remove any traces of unbound PAB. 3 M NaOAc (pH 5.6) is added to the DNA solution to a final concentration of 0.3 M and the labeled DNA is precipitated by the addition of three volumes of ethanol.

After the sample is cooled at -70°C for 15 minutes, the precipitated DNA is recovered by centrifugation for 10 minutes. The DNA pellet is dissolved in 10 mM Tris (pH 7.9) and 0.1 mM EDTA. The labeled probe DNA remains stable for one year if stored at -20°C.

A non-radioactive method of labeling the DNA probes may be desirable because: (1) the photoactivatable reactions are simple and rapid, (2) the sensitivity is as high as ³²P-labeled probes,

(3) the PAB-labeled probes have a long storage life, (4) these probes are relatively inexpensive, and (5) detection of bound probes is by simple colorimetric methods. The radioactive labeling of probes requires the use of ^{32}P , which has a very short half-life (14 days) and is thus unstable and expensive. The use of radioactive probes would be limited because of cost, the dangers of radioactivity, strict requirements for disposal, and the need for licensing. However, if for some reason the biotin-HRP method of labeling is unacceptable, the DNA fragments can be labeled with [δ P] 32 deoxy-CTP by standard nick translation methods as described by Maniatis *et al.* (1982, *supra*). Other labelling techniques which are well known or accepted by ordinary skilled artisans can also be employed for visualization of the nucleic acid probes.

Example 15 - Determining the Specificity of the DNA Probes

The prepared DNA probes are screened for specificity against a battery of oral *Porphyromonas* species, other oral species, and other non-oral gram-negative bacteria.

Cultures of the test strains are grown in appropriate medium to a density of approximately 10^9 cells per ml. The cells are centrifuged and suspended in 5.0 ml of distilled water. Sodium hydroxide is added to 0.5 N and the cells are incubated at 90°C for 20 to 30 minutes in order to lyse the cells and denature the DNA. The cell suspension is neutralized by the addition of 0.5 N HCl diluted in 20x SSC and chilled on ice for 20 minutes. A volume of 0.5 ml (or less) of the suspension is diluted to 4.0 ml volume with 10x SSC and vacuum filtered in a manifold onto nitrocellulose paper (type HAWP, 0.45 μm , Millipore Corp.) which is prewetted with 10x SSC. After the filters are rinsed with 4.0 ml of 10x SSC, they are dried and heated at 85°C for 3 hours in a vacuum oven (this fixes the chromosomal DNA onto the filter). After the filters are incubated for 2-3 hours at 42°C with the prehybridization buffer (6x SSPE [1.08 M NaCl, 0.06 M NaH_2PO_4 , 0.48 M NaOH, 6.0 mM Na_2EDTA , pH 7.0], 5x BFP [0.1% BSA, 0.1% Ficoll, and 0.1% polyvinyl pyrrolidone], 1% [w/v] glycine, 50% formamide, and 100 μg denatured salmon sperm DNA/ml), the prehybridization buffer is replaced with hybridization buffer containing 0.01 to 0.1 μg of labeled heat-denatured probe DNA in 5x SSPE, 1x BFP, 50% formamide, 100 μg salmon sperm/ml, 0.3% SDS, and 10% sulfate. Hybridization is accomplished by incubating the DNA mixtures for 12 hours at 42°C . The filters are then washed twice in 2x SSPE - 0.2% SDA for 25 minutes at 60°C in order to remove any unhybridized probe DNA.

The hybridized (bound) probe DNA can be detected by incubation of the filters for 30 minutes on 1 M NaCl + 0.1 M Tris-HCl (pH 7.5) + 2 mM MgCl_2 + 0.05% "TRITON" X-100 + 3% BSA and then for 25 minutes in 1 mg/ml streptavidin alkaline phosphate conjugate in the same buffer. Next, the filters are washed 3 times with 50-100 ml of buffer containing 1 M NaCl, 0.1 M

Tris-HCl, pH 7.5, 2 mM MgCl₂, and 0.05% "TRITON" X-100. A fourth wash of buffer contains 0.1 M NaCl and 0.3 M sodium citrate, pH 7.0. The color is developed by the addition of 32 µl nitroblue tetrazolium, 16 µl 5-bromo-4-chloro-3-indosyl-phosphate in 5.0 ml of 0.1 M NaCl + 0.3 M sodium citrate. After incubation in subdued light for 30 minutes, any spots which are visible indicate hybridization of probe DNA to target DNA.

If ³²P-labeled probes are used the same hybridization conditions can be used (adding 10⁶ CPM of ³²P probe) but instead of adding the streptavidin conjugate, the filters are dried for 1-2 hours at 70°C, and hybridization is detected by autoradiography. Alternatively, the filters can be cut into squares, placed into scintillation vials, and counted in scintillant.

Once probes are identified which are specific for either *B. intermedius* or *P. gingivalis*, or several *Porphyromonas* spp., they can be tested with known mixtures of the test bacteria grown on plates as follows: various mixtures of the test bacteria can be prepared with a known concentration of *B. intermedius* or *P. gingivalis* and spread on agar plates and incubated anaerobically as described earlier in this proposal. After the colonies have appeared (2-4 days), they are blotted onto nitrocellulose membranes, and the membranes processed for hybridization. If the DNA probe(s) is specific and sensitive, then only the *P. gingivalis* or *B. intermedius* colony blots should be positive. It is also possible that a probe may be found that is genus or group specific.

DNA probes for chromosomally-encoded genes require 10⁵ to 10⁶ bacteria per colony or dot blot in order to give a reliable positive result. This is comparable to 1 to 10 pg of DNA. Given this level of detection, a primary culturing step is desirable prior to blotting the colonies onto membrane filters and hybridization with the probe DNA.

Example 16 - Vaccines

In view of the immunoprotectant activity exhibited by certain of the compositions of matter of the subject invention, vaccines may be produced from the polypeptides expressed by cells which have been transformed with DNA fragments from *Porphyromonas gingivalis*. By introducing these peptides, along with a pharmacologically suitable vehicle, into the human or animal host, that host can be induced to generate immunological protection against *P. gingivalis*. The preparation of such a vaccine composition is within the skill of one trained in the medical and immunological sciences. Cells which can be used to produce recombinant peptides include, but are not limited to, bacteria, yeasts, insects, and eukaryotic cells.

Example 17 - Construction of an Oral Vaccine

It has been recognized that natural infection with enteric organisms produces the highest levels of antibodies and the longest lasting immunity to reinfection. The use of *Salmonella* as an attenuated vaccine carrier organism has several advantages. *Salmonella* spp. are capable of colonizing the Peyer's patches and gut lamina propria where they elicit a strong local IgA response in the intestine. The IgA response is also spread to other external secretions such as saliva by the seeding of these tissues with plasma cell precursors primed in the gut via the so called common mucosal immune system. These responses are important in preventing initial adhesion and colonization of mucosal surfaces - the initial step in the etiology of periodontal disease. In addition, live *Salmonella* elicits a humoral (serum) response of the IgM, IgG and IgA isotypes due to its invasive nature. Finally, infection with live organisms also stimulates a cell-mediated immune response—primarily T-cell mediated stimulation of macrophages—which is important in immunity since *Salmonella* can survive intracellularly within phagocytic cells. Several non-virulent mutants of *Salmonella* spp. have been developed. For example, an attenuated *galE* mutant of *S. typhi* (strain Ty21a) which lacks the enzyme UDP-galactose-4-epimerase has been developed.

Another approach to attenuation has been to use aromatic amino acid dependent (*aro*⁻) strains of *Salmonella* which are nonvirulent because they require metabolites not found in mammalian tissues, i.e., *p*-aminobenzoate and 2,3-dihydroxybenzoate. The strains are constructed using the *aro*:A554::Tn10 transposon, and, because it can cause deletion or deletion-inversion mutations, one can generate non-reverting mutants. These mutants synthesize a complete smooth LPS, are able to effectively colonize the Peyer's patches and gut, and are highly immunogenic. In mice of the *Salmonella*-susceptible line BALB/c, intraperitoneal injection of as few as 2×10^5 *aro*⁻ *S. typhimurium* protected against an i.p. challenge of 5×10^5 virulent parent cells 30 days later ($>25,000$ i.p.LD₅₀). Oral immunization with 2×10^8 *aro*⁻ cells protected mice against an oral challenge of 3×10^7 virulent organisms (ca. 100 oral LD₅₀).

Because live *Salmonella* is such an efficient stimulator of mucosal immunity it can be used as a carrier to deliver recombinant gene products cloned from other pathogens directly to the tissues (i.e., Peyer's patches) which most efficiently generate an immune response in the gut, and through the common mucosal immune system, to other distant secretory sites. At the same time a humoral immune response is stimulated which may further help prevent or abort invasion. Using cloned antigens in a *Salmonella* carrier system gives one the ability to target the immune response to important virulence antigens leading to a protective immune response.

Chromosomal DNA was isolated from *P. gingivalis* strain 381 by the following method: One to three liters of cells were pelleted by centrifugation and washed (on ice) in 1/50 volume of 1X

SSC buffer (0.87% NaCl, 0.04% Na citrate) containing 27% sucrose and 10 mM EDTA. The cells were again pelleted and resuspended to 10^{10} cells/ml in the same buffer. Lysozyme (5 mg/ml in 1X SSC buffer) was added to 0.5 mg/ml, the cells were mixed thoroughly and incubated at 37°C for 10 minutes. Nine volumes of 1X SSC containing 27% sucrose, 10 mM EDTA and 1.11% SDS (prewarmed to 39°C) were added to the cells and incubated at 37°C until cell lysis was complete (10-30 minutes). The lysed cells were mixed gently and incubated at 37°C for 30 minutes. Proteinase K (Sigma, St. Louis, MO) was added to a final concentration of 1 mg/ml and the lysate was incubated at 37°C for 4 hours. An equal volume of phenol-Tris (9:1 freshly distilled phenol: 1 M Tris-HCl, pH 7.5) was added to the Proteinase K-treated mixture and the mixture was agitated gently at room temperature for 30 minutes. The DNA mixture was then centrifuged in 150 ml Corex tubes at 3000 rpm. The top (phenol) layer was removed and discarded. The phenol extraction was repeated and the DNA (aqueous) layer was dialyzed extensively against 10 mM Tris-HCl, pH 8.0, 1 mM EDTA. Finally, the DNA was incubated with RNase at 37°C for 1 hour.

Expression vectors which contain a promoter upstream from the cloning site were used to help insure that cloned DNA was expressed whether or not a structural gene was cloned with its own promoter. The expression plasmid pUC9 (2.7 kb) contains the origin of replication, ampicillin resistance gene, and *lac* gene of pBR 322. The *lac* *Hae*II fragment (*lac* gene) contains a polylinker region from M12mp9 which has multiple unique cloning sites in the gene that encodes for the peptide of β -galactosidase. Thus, recombinant vectors that contain an insert in any of the cloning sites generate white colonies on X-GAL plates since they are not able to degrade the lactose analog, X-GAL. Vectors without an insert degrade X-GAL and result in blue colonies on X-GAL plates since the gene is not interrupted by an insert. Other plasmid vectors are available and could be used. One such plasmid is pAD 230.

The chromosomal DNA and vector DNA were ligated with T4 DNA ligase at ratios of 2:1 and 5:1. The ligated DNA was phenol-chloroform (24:1 isoamyl alcohol) extracted, ethanol precipitated, washed, dried, and redissolved in TE. Early log-phase cells (OD=0.2 to 0.5) were washed with transformation buffer 1 (TFM 1, 10 mM Tris-Cl, pH 7.5, 0.15 M NaCl). The cells were pelleted, resuspended, and incubated on ice for 45 minutes in TFM 2 (50 mM CaCl_2). After the cells are again pelleted, they are gently resuspended once more in TFM 2. A 0.2 ml volume of cells were added to 0.1 ml TFM 3 (10 mM Tris-HCl, pH 7.5, 50 mM CaCl_2 , 10 mM $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$) on ice. Varying amounts of DNA were added to the cells. The tubes were incubated on ice for 45 minutes, at which time the cells were heat shocked at 37°C for 2 minutes. A 0.5 ml volume of LB broth was added per tube and the cells were incubated at 37°C for 30 to 60 minutes to allow

expression of antibiotic resistance. Finally, the cells were spread on plates of LB + antibiotic (50 µg/ml ampicillin) and X-GAL and incubated 24 to 48 hours at 37°C.

Any colonies which appeared on the LB + ampicillin + X-GAL plates after 24-36 hours of incubation were transformants which contained and expressed pUC9. A large number (80-90%) of these were white colonies which contain a plasmid with inserted *P. gingivalis* DNA. Once a transformant was identified which expressed *P. gingivalis* SHA adhesin, the protein was identified by Western blotting cell lysates of the transformant.

Because the initial cloning was done in *E. coli*, the recombinant plasmids may be modified by the *E. coli* modification system. These modified recombinant plasmids were used to transform strains of *Salmonella*. Initially, recombinant plasmids were passed into *Salmonella typhimurium* strain LB 5000, which is restriction⁺ (is not able to restrict foreign DNA) but modification⁻. This modifies the plasmid DNA according to the *Salmonella* system.

Recombinant *P. gingivalis* plasmids encoding for the *Porphyromonas* (SHA) adhesin can be isolated and purified as described above. The identity and purity of the preparation can be monitored by restriction analysis and agarose gel electrophoresis. Cells of *Salmonella* strain LB 5000 can be made competent and transformed with the recombinant plasmid as described above. Transformants can be selected by growth in the presence of ampicillin and are tested for the expression of the *Porphyromonas* antigen also by procedures described above.

The recombinant plasmid can be isolated from strain LB 5000 and the identity of the plasmid verified. The purified plasmid can be used to transform non-reverting nonvirulent mutants of various *Salmonella* spp. These strains include (but are not limited to) *S. enteritidis* (*typhimurium*) SL 3261 (WRAY *his* G46 *aro* A), SL 1479 (UCD *his* C527 *aro* A), SL 3237 (FIRN *rps* L120 *aro* A), and *S. dublin* SL 3261 (*his* 646 *aro* A). Transformants can be screened for resistance to ampicillin and assayed for expression of the *Porphyromonas* antigen by enzyme-linked immunosorbent assay as described above. In addition, SDS-PAGE and Western blotting can be done to confirm the presence of the antigen in the *Salmonella* transformants.

The *P. gingivalis* hemagglutinin protein was expressed in nonvirulent *Salmonella typhimurium* strain SL3261/CL7 and tested for activity as a competitive inhibitor of hemagglutination. The *S. typhimurium* cells were broken by sonic disruption, whole cells and debris removed by centrifugation and the supernatant adjusted to 40% saturation with NH_4SO_4 . The supernatant was collected, dialyzed, and fractionated on a CM-Sephadex column using a 50-450 mM NaCl gradient. Fractions were evaluated via Western blot analysis for reactivity with absorbed sera directed against *P. gingivalis*. The peak fraction was found to inhibit hemagglutination of

erythrocytes by whole *P. gingivalis* cells. This same material was analyzed for the N-terminal amino acid sequence and found to match the sequence predicted from the cloned gene.

5 The gene for the *Porphyromonas* antigen can also be transduced into the *Salmonella* carrier strains by P22 transduction. Transductants can be selected by growth in the presence of ampicillin and by the expression of the *Porphyromonas* antigen, as detected by immunoblotting using the monospecific or monoclonal antibody.

10 Additional carrier strains can be generated from other *Salmonella* serotypes. These strains can be derived from virulent strains by the introduction of mutations such as (auxotrophic) *aro* A or *gal* E. In addition, the "O" antigen may be altered or mutated to a rough LPS in strains already avirulent by P₁ transduction.

Example 18 - Monoclonal Antibodies

15 Appropriate mice can be immunized with antigens of, or cells expressing antigens of, *Porphyromonas gingivalis*. The antigens used for this immunization can be those which are identified and described in the previous examples in view of their exhibited immunogenic activity. The techniques employed to accomplish this immunization procedure are familiar to those skilled in this art. The spleens can then be removed from the immunized mice and the cells therefrom fused to SP-2 myeloma cells using polyethylene glycol. The desired hybrid cells can then be selected by adding hypoxanthine-aminopterin-thymidine to the medium. The surviving cells can then be tested for antibody production. The testing for antibody production can be accomplished using ELISA, immunoblot, and/or Western blot procedures as described in the previous examples.

20 The monoclonal antibodies produced by the procedure just described can be used to test for the presence of *P. gingivalis* antigens in a sample of biological fluid. The testing procedure involves contacting the biological fluid with a composition containing one or more of the monoclonal antibodies. If *P. gingivalis* antigens are present in the biological fluid, then a reaction will occur and this reaction can be detected and quantified by fluorescence or other means.

25 It should be understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and the scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT(S) INFORMATION:

Applicant Name: University of Florida
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City: Gainesville
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Applicant Name: University of Alabama-Birmingham Research Foundation
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City: Birmingham
State/Province: Alabama
Country: US
Postal code/Zip: 35294
Phone number: (205) 934-9911 Fax: (205) 975-5560

(ii) TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
and Probes for the Detection of Periodontal Disease

(iii) NUMBER OF SEQUENCES: 29

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Ted W. Whitlock
(B) STREET: 2421 N.W. 41st Street, Suite A-1
(C) CITY: Gainesville
(D) STATE: FL
(E) COUNTRY: USA
(F) ZIP: 32606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/353,485
(B) FILING DATE: 09-DEC-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/647,119
(B) FILING DATE: 25-JAN-1991
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/241,640
(B) FILING DATE: 08-SEP-1988

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Whitlock, Ted W.

(B) REGISTRATION NUMBER: 36,965
(C) REFERENCE/DOCKET NUMBER: UF15.C3

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4510 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 27..1518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Leu Ala Val Leu Leu Ser Leu Leu Cys Trp Gly Gln Thr Ala Ala Ala	
10 15 20 25	
CAG GGA GGG CCG AAG ACT GCT CCT TCT GTG ACG CAC CAA GCG GTG CAG	149
Gln Gly Gly Pro Lys Thr Ala Pro Ser Val Thr His Gln Ala Val Gln	
30 35 40	
AAA GGT ATT CGA ACA TCC AAG GTT AAG GAT CTC CGA GAT CCG ATT CCT	197
Lys Gly Ile Arg Thr Ser Lys Val Lys Asp Leu Arg Asp Pro Ile Pro	
45 50 55	
GCC GGT ATG GCA CGA ATT ATC TTG GAG GCT CAC GAT GTA TGG GAA GAC	245
Ala Gly Met Ala Arg Ile Ile Leu Glu Ala His Asp Val Trp Glu Asp	
60 65 70	
GGC ACA GGC TAT CAA ATG CTT TGG GAT GCA GAT CAC AAT CAG TAC GGC	293
Gly Thr Gly Tyr Gln Met Leu Trp Asp Ala Asp His Asn Gln Tyr Gly	
75 80 85	
GCA TCC ATT CCC GAA GAA TCT TTT TGG TTT GCC AAC GGA ACG ATC CCG	341
Ala Ser Ile Pro Glu Glu Ser Phe Trp Phe Ala Asn Gly Thr Ile Pro	
90 95 100 105	
GCC GGT CTT TAC GAT CCT TTC GAG TAT AAA GTT CCG GTC AAT GCC GAT	389
Ala Gly Leu Tyr Asp Pro Phe Glu Tyr Lys Val Pro Val Asn Ala Asp	
110 115 120	
GCA TCT TTT TCT CCC ACG AAT TTC GTG CTT GAT GGA ACA GCA TCA GCC	437
Ala Ser Phe Ser Pro Thr Asn Phe Val Leu Asp Gly Thr Ala Ser Ala	
125 130 135	
GAT ATT CCT GCC GGC ACT TAT GAC TAT GTA ATC ATT AAC CCC AAT CCT	485
Asp Ile Pro Ala Gly Thr Tyr Asp Tyr Val Ile Ile Asn Pro Asn Pro	
140 145 150	

48

GGC ATA ATA TAT ATA GTA GGA GAG GGT GTC TCC AAA GGT AAC GAT TAT Gly Ile Ile Tyr Ile Val Gly Glu Gly Val Ser Lys Gly Asn Asp Tyr 155 160 165	533
GTG GTA GAG GCC GGT AAG ACT TAT CAT TTC ACT GTC CAA CGA CAA GGC Val Val Glu Ala Gly Lys Thr Tyr His Phe Thr Val Gln Arg Gln Gly 170 175 180 185	581
CCC GGC GAT GCT GCG TCC GTT GTA GTG ACC GGA GAA GGT GGC AAT GAA Pro Gly Asp Ala Ala Ser Val Val Thr Gly Glu Gly Gly Asn Glu 190 195 200	629
TTC GCT CCC GTA CAG AAT CTC CAA TGG TCT GTA TCT GGG CAG ACA GTG Phe Ala Pro Val Gln Asn Leu Gln Trp Ser Val Ser Gly Gln Thr Val 205 210 215	677
ACC CTC ACT TGG CAA GCC CCC GCA TCC GAC AAA CGG ACT TAT GTG TTG Thr Leu Thr Trp Gln Ala Pro Ala Ser Asp Lys Arg Thr Tyr Val Leu 220 225 230	725
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GCT CCC GGC CAG TAT AAC TAC TGT GTT GAA GTT AAG TAC ACA GCC GGC Ala Pro Gly Gln Tyr Asn Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly 445 450 455	1397
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 497 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Pro Ser Val Thr His Gln Ala Val Gln Lys Gly Ile Arg Thr Ser Lys
          35           40           45
Val Lys Asp Leu Arg Asp Pro Ile Pro Ala Gly Met Ala Arg Ile Ile
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Leu Glu Ala His Asp Val Trp Glu Asp Gly Thr Gly Tyr Gln Met Leu
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Trp Asp Ala Asp His Asn Gln Tyr Gly Ala Ser Ile Pro Glu Glu Ser
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Phe Trp Phe Ala Asn Gly Thr Ile Pro Ala Gly Leu Tyr Asp Pro Phe
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Glu Tyr Lys Val Pro Val Asn Ala Asp Ala Ser Phe Ser Pro Thr Asn
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Phe Val Leu Asp Gly Thr Ala Ser Ala Asp Ile Pro Ala Gly Thr Tyr
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Asp Tyr Val Ile Ile Asn Pro Asn Pro Gly Ile Ile Tyr Ile Val Gly
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Glu Gly Val Ser Lys Gly Asn Asp Tyr Val Val Glu Ala Gly Lys Thr
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Tyr His Phe Thr Val Gln Arg Gln Gly Pro Gly Asp Ala Ala Ser Val
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Val Val Thr Gly Glu Gly Gly Asn Glu Phe Ala Pro Val Gln Asn Leu
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Thr Leu Pro Asn Gly Trp Thr Met Ile Asp Ala Asp Gly Asp Gly His
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52

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 370 375 380
 Val Tyr Leu Ala Phe Arg His Phe Asn Ser Thr Gly Ile Phe Arg Leu
 385 390 395 400
 Tyr Leu Asp Asp Val Ala Val Ser Gly Glu Gly Ser Ser Asn Asp Tyr
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 435 440 445
 Cys Val Glu Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Val Cys Lys
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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1470 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*
 (B) STRAIN: FDC381

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: genomic
 (B) CLONE: ST7

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 310..1359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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ACGGCTGTTT TGACCTTTCG TCGCTGACA ATGCTTATAT AAAAGCTGTT TCAGGGGGCA	240
GTGTCACTTG ACACTGCTAC CAATAACAGA TTAATAATCA ATCAAATACA ACAAAAAAAG	300
GAAAAACAA ATG ACT GTA GAA AAT TTG CGT CTG CAG CGG CTC CAA AAT	348
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1 5 10	
TTG GAG CAC TAC CGT TTT GCC AAG AAT GTG CTG ACG CTC TGT CGC ACG	396
Leu Glu His Tyr Arg Phe Ala Lys Asn Val Leu Thr Leu Cys Arg Thr	
15 20 25	
GCA AAT ATC GCT AAA CTG AAT CCC AAA CTG CCC GAG CTG GAA AAG GCT	444
Ala Asn Ile Ala Lys Leu Asn Pro Lys Leu Pro Glu Leu Glu Lys Ala	
30 35 40 45	
ATC GAA ATG GAG GAT TTG GCT CTG AAT CCG CCC GTC GCG AAC GAG CTG	492
Ile Glu Met Glu Asp Leu Ala Leu Asn Pro Pro Val Ala Asn Glu Leu	
50 55 60	
ACG CCT CAG GTC ATA GCC CTC GAC GAG GAA CGC GAC AGA GCC TAT CAG	540
Thr Pro Gln Val Ile Ala Leu Asp Glu Glu Arg Asp Arg Ala Tyr Gln	
65 70 75	
GCG CTG ATG TCG CGC GTG CGT TCG TAT GCT TTC GAC GAG GAC AGC CAG	588
Ala Leu Met Ser Arg Val Arg Ser Tyr Ala Phe Asp Glu Asp Ser Gln	
80 85 90	
CTG CGC AAC GCG GCA GCC AGA ATC GAA GAC GTG GCC GCT CGC TAC GGC	636
Leu Arg Asn Ala Ala Ala Arg Ile Glu Asp Val Ala Ala Arg Tyr Gly	
95 100 105	
AAC GTG ATC CGA ATG AAC TAT GAC AAG GAG ACG GCC GCG ATA GAG AAT	684
Asn Val Ile Arg Met Asn Tyr Asp Lys Glu Thr Ala Ala Ile Glu Asn	
110 115 120 125	
TTC CTC ACC GAT CTC AAG GGC GAG AAC ATT CGC CCC CTC GTA ACG AAA	732
Phe Leu Thr Asp Leu Lys Gly Glu Asn Ile Arg Pro Leu Val Thr Lys	
130 135 140	

54

CTC GGC GTG ACG GCA CTC GTT GAC AGA CTG GAA AAG AAC AAT AAG GCC Leu Gly Val Thr Ala Leu Val Asp Arg Leu Glu Lys Asn Asn Lys Ala 145 150 155	780
TTC GCC GAC TTC TTC CTC CGC CGT CTG AGC ACC GAC CAA CGA GGC AAA Phe Ala Asp Phe Phe Leu Arg Arg Leu Ser Thr Asp Gln Arg Gly Lys 160 165 170	828
TAT GAC GTG AAG GCA CTC CGT GCC GAG ACC GAC CGC ACA TTG GTA GCC Tyr Asp Val Lys Ala Leu Arg Ala Glu Thr Asp Arg Thr Leu Val Ala 175 180 185	876
GTG GTG CGC CGC ATG GAC TCC ATC GAC GAC ATG GAG CCG AGC CCG GAG Val Val Arg Arg Met Asp Ser Ile Asp Asp Met Glu Pro Ser Pro Glu 190 195 200 205	924
ATC CGT GCG CTC ATC GAG CTC TAC AAC CGA CTC GTG GCC AAT CGC CGC Ile Arg Ala Leu Ile Glu Leu Tyr Asn Arg Leu Val Ala Asn Arg Arg 210 215 220	972
GCT CTC TTG GCT CGT CGC GCC AGC TAC GGA GAA GCA GCC GTG GAG AAG Ala Leu Leu Ala Arg Arg Ala Ser Tyr Gly Glu Ala Ala Val Glu Lys 225 230 235	1020
CGT CGT GCC GAG ATC GCC GAG ATG CTC CGC CCC CTG CTC GCC CGG ATC Arg Arg Ala Glu Ile Ala Glu Met Leu Arg Pro Leu Leu Ala Arg Ile 240 245 250	1068
GTG GAG GAG AAG AAG ACG GCC GTC TTT GCC GGT CGC ACC CTC GGC ACG Val Glu Glu Lys Lys Thr Ala Val Phe Ala Gly Arg Thr Leu Gly Thr 255 260 265	1116
GGC AAG AAC CGC CAC TAT CTC ATC ACA TTC GTA GCC GAG AAC GGC GAC Gly Lys Asn Arg His Tyr Leu Ile Thr Phe Val Ala Glu Asn Gly Asp 270 275 280 285	1164
GAG GAG GAT CGC TGG TAC CGC ATC AAC GGG GAG CAA CTC GTC TAT GTG Glu Glu Asp Arg Trp Tyr Arg Ile Asn Gly Glu Gln Leu Val Tyr Val 290 295 300	1212
CCC GAA GAC GAA CTC CCC AAG CCG AAG AAA AAG AAG AAA CCC GCA AGC Pro Glu Asp Glu Leu Pro Lys Pro Lys Lys Lys Lys Pro Ala Ser 305 310 315	1260
AGC ACG GAC ACT CCA TCC GAG CCG CCC GTC CTG CCG GAT CCA TCG CAA Ser Thr Asp Thr Pro Ser Glu Pro Pro Val Leu Pro Asp Pro Ser Gln 320 325 330	1308
GGA GGC AGC AGT AGC GGC GGT GGC GAG CAA GGC TCT ACC GGC GGC GGA Gly Gly Ser Ser Ser Gly Gly Glu Gln Gly Ser Thr Gly Gly Gly 335 340 345	1356
CTC TGATCCCCC GTGCCGTCCT GCCGGCCGCA GCAGCACAGG CAACCGAGTA Leu 350	1409
TAAAGACAA AGGGGCTGTG ACCAAATTCA TTTTGGCAC AGCCCCTTGT ATATTCGAAA A	1469 1470

55

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Thr Val Glu Asn Leu Arg Leu Gln Arg Leu Gln Asn Leu Glu His
 1             5             10             15
Tyr Arg Phe Ala Lys Asn Val Leu Thr Leu Cys Arg Thr Ala Asn Ile
      20             25             30
Ala Lys Leu Asn Pro Lys Leu Pro Glu Leu Glu Lys Ala Ile Glu Met
      35             40             45
Glu Asp Leu Ala Leu Asn Pro Pro Val Ala Asn Glu Leu Thr Pro Gln
      50             55             60
Val Ile Ala Leu Asp Glu Glu Arg Asp Arg Ala Tyr Gln Ala Leu Met
      65             70             75             80
Ser Arg Val Arg Ser Tyr Ala Phe Asp Glu Asp Ser Gln Leu Arg Asn
      85             90             95
Ala Ala Ala Arg Ile Glu Asp Val Ala Ala Arg Tyr Gly Asn Val Ile
      100            105            110
Arg Met Asn Tyr Asp Lys Glu Thr Ala Ala Ile Glu Asn Phe Leu Thr
      115            120            125
Asp Leu Lys Gly Glu Asn Ile Arg Pro Leu Val Thr Lys Leu Gly Val
      130            135            140
Thr Ala Leu Val Asp Arg Leu Glu Lys Asn Asn Lys Ala Phe Ala Asp
      145            150            155            160
Phe Phe Leu Arg Arg Leu Ser Thr Asp Gln Arg Gly Lys Tyr Asp Val
      165            170            175
Lys Ala Leu Arg Ala Glu Thr Asp Arg Thr Leu Val Ala Val Val Arg
      180            185            190
Arg Met Asp Ser Ile Asp Asp Met Glu Pro Ser Pro Glu Ile Arg Ala
      195            200            205
Leu Ile Glu Leu Tyr Asn Arg Leu Val Ala Asn Arg Arg Ala Leu Leu
      210            215            220
Ala Arg Arg Ala Ser Tyr Gly Glu Ala Ala Val Glu Lys Arg Arg Ala
      225            230            235            240
Glu Ile Ala Glu Met Leu Arg Pro Leu Leu Ala Arg Ile Val Glu Glu
      245            250            255
Lys Lys Thr Ala Val Phe Ala Gly Arg Thr Leu Gly Thr Gly Lys Asn
      260            265            270

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Arg His Tyr Leu Ile Thr Phe Val Ala Glu Asn Gly Asp Glu Glu Asp
 275 280 285

Arg Trp Tyr Arg Ile Asn Gly Glu Gln Leu Val Tyr Val Pro Glu Asp
 290 295 300

Glu Leu Pro Lys Pro Lys Lys Lys Lys Pro Ala Ser Ser Thr Asp
 305 310 315 320

Thr Pro Ser Glu Pro Pro Val Leu Pro Asp Pro Ser Gln Gly Gly Ser
 325 330 335

Ser Ser Gly Gly Gly Glu Gln Gly Ser Thr Gly Gly Gly Leu
 340 345 350

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1841 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 374..1424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGCTTGAC CTACGACAAA AGATTTTTTC ATCTTACTAT ATTTTGGGAT TATATTTCTA 60

CACCTCCTTA TCCGGAATTT GGAAATGCGG GGCAAAAGTA GAAAAATTTT ATTTCCATCA 120

AAAAAAATCT TCAAATTTTT TTCACCTTGC GCATTCTGCA TATAAATGCT GCTACGTCGG 180

CAGATTATTC TGGTTAAAAA GTTATAGATG CAGCTCTTGG TTATAGTGTC CTAAGATCGC 240

TATGCAACCT GTAAGAAACG ATTGTAGGGT GTTCTTGCT TCCTGCACGA ATGCAGGAGA 300

GCAGAAACGC CCGTTGCTGC TCCCGTCAAT AACTAATTA TTATCGACTT AACCCCTTAA 360

TTCAAAAAC TAA ATG ACT GCA GAA ATT TTC TCG TTT TCC CGG CTC CAA 409
 Met Thr Ala Glu Ile Phe Ser Phe Ser Arg Leu Gln
 1 5 10

AAT TTG GAG CAC TAC CGT TTT GCC AAG AAT GTG CTG ACG CTC TGT CGC 457
 Asn Leu Glu His Tyr Arg Phe Ala Lys Asn Val Leu Thr Leu Cys Arg
 15 20 25

ACG GCA AAT ATC GCT AAA CTG AAT CCC AAA CTG CCC GAG CTG GAA AAG 505
 Thr Ala Asn Ile Ala Lys Leu Asn Pro Lys Leu Pro Glu Leu Glu Lys
 30 35 40

GCT ATC GAA ATG GAG GAT TTG GCT CTG AAT CCG CCC GTC GCG AAC GAG 553
 Ala Ile Glu Met Glu Asp Leu Ala Leu Asn Pro Pro Val Ala Asn Glu
 45 50 55 60

57

CTG ACG CCT CAG GTC ATA GCC CTC GAC GAG GAA CGC GAC AGA GCC TAT Leu Thr Pro Gln Val Ile Ala Leu Asp Glu Glu Arg Asp Arg Ala Tyr 65 70 75	601
CAG GCG CTG ATG TCG CGC GTG CGT TCG TAT GCT TTC GAC GAG GAC AGC Gln Ala Leu Met Ser Arg Val Arg Ser Tyr Ala Phe Asp Glu Asp Ser 80 85 90	649
CAG CTG CGC AAC GCG GCA GCC AGA ATC GAA GAC GTG GCC GCT CGC TAC Gln Leu Arg Asn Ala Ala Ala Arg Ile Glu Asp Val Ala Ala Arg Tyr 95 100 105	697
GGC AAC GTG ATC CGA ATG AAC TAT GAC AAG GAG ACG GCC GCG ATA GAG Gly Asn Val Ile Arg Met Asn Tyr Asp Lys Glu Thr Ala Ala Ile Glu 110 115 120	745
AAT TTC CTC ACC GAT CTC AAG GGC GAG AAC ATT CGC CCC CTC GTA ACG Asn Phe Leu Thr Asp Leu Lys Gly Glu Asn Ile Arg Pro Leu Val Thr 125 130 135 140	793
AAA CTC GGC GTG ACG GCA CTC GTT GAC AGA CTG GAA AAG AAC AAT AAG Lys Leu Gly Val Thr Ala Leu Val Asp Arg Leu Glu Lys Asn Asn Lys 145 150 155	841
GCC TTC GCC GAC TTC TTC CTC CGC CGT CTG AGC ACC GAC CAA CGA GGC Ala Phe Ala Asp Phe Phe Leu Arg Arg Leu Ser Thr Asp Gln Arg Gly 160 165 170	889
AAA TAT GAC GTG AAG GCA CTC CGT GCC GAG ACC GAC CGC ACA TTG GTA Lys Tyr Asp Val Lys Ala Leu Arg Ala Glu Thr Asp Arg Thr Leu Val 175 180 185	937
GCC GTG GTG CGC CGC ATG GAC TCC ATC GAC GAC ATG GAG CCG AGC CCG Ala Val Val Arg Arg Met Asp Ser Ile Asp Asp Met Glu Pro Ser Pro 190 195 200	985
GAG ATC CGT GCG CTC ATC GAG CTC TAC AAC CGA CTC GTG GCC AAT CGC Glu Ile Arg Ala Leu Ile Glu Leu Tyr Asn Arg Leu Val Ala Asn Arg 205 210 215 220	1033
CGC GCT CTC TTG GCT CGT CGC GCC AGC TAC GGA GAA GCA GCC GTG GAG Arg Ala Leu Leu Ala Arg Arg Ala Ser Tyr Gly Glu Ala Ala Val Glu 225 230 235	1081
AAG CGT CGT GCC GAG ATC GCC GAG ATG CTC CGC CCC CTG CTC GCC CGG Lys Arg Arg Ala Glu Ile Ala Glu Met Leu Arg Pro Leu Leu Ala Arg 240 245 250	1129
ATC GTG GAG GAG AAG AAG ACG GCC GTC TTT GCC GGT CGC ACC CTC GGC Ile Val Glu Glu Lys Lys Thr Ala Val Phe Ala Gly Arg Thr Leu Gly 255 260 265	1177
ACG GGC AAG AAC CGC CAC TAT CTC ATC ACA TTC GTA GCC GAG AAC GGC Thr Gly Lys Asn Arg His Tyr Leu Ile Thr Phe Val Ala Glu Asn Gly 270 275 280	1225
GAC GAG GAG GAT CGC TGG TAC CGC ATC AAC GGG GAG CAA CTC GTC TAT Asp Glu Glu Asp Arg Trp Tyr Arg Ile Asn Gly Glu Gln Leu Val Tyr 285 290 295 300	1273

58

GTG CCC GAA GAC GAA CTC CCC AAG CCG AAG AAA AAG AAG AAA CCC GCA 1321
 Val Pro Glu Asp Glu Leu Pro Lys Pro Lys Lys Lys Lys Lys Pro Ala
 305 310 315
 AGC AGC ACG GAC ACT CCA TCC GAG CCG CCC GTC CTG CCG GAT CCA TCG 1369
 Ser Ser Thr Asp Thr Pro Ser Glu Pro Pro Val Leu Pro Asp Pro Ser
 320 325 330
 CAA GGA GGC AGC AGT AGC GGC GGT GGC GAG CAA GGC TCT ACC GGC GGC 1417
 Gln Gly Gly Ser Ser Ser Gly Gly Gly Glu Gln Gly Ser Thr Gly Gly
 335 340 345
 GGA CTC T GATCCGCACT CCCCCGTGCC GTCCTGTCGG CCGCAGCAGC ACAGGCAACC 1474
 Gly Leu
 350
 GAGTATAAAA GACAAAGGGG CTGTGACCAA ATTCATTTTT GGCACAGCCC CTTTCAGGTG 1534
 CATAAGAATC TATATTACGG GAGAACAATC CCTGTAAGAG CAGTCACGAT GCCGTTTTCC 1594
 TCATATACAG TAATCCGGAA GACGTCTTCC AGCAGATCGG GATGTCTCAG AACCCATGCT 1654
 CCTTTTATGG GCTGGGGTTT TGGTTTGGCT CTGTAAATTT TTCCAAGGGA TCTAGTTTTT 1714
 AGCTCTCAAT GGGCCAGATC CCCCCTCAAG TGCAATTCGA GAGAGGATAA AAGGGATAAT 1774
 CCGTGAACGC TCTGCGGTCT ATCGGTAGCG TACGGTCATG AACAGGTGTG TACGTGCCTG 1834
 TCCGCGG 1841

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Ala Glu Ile Phe Ser Phe Ser Arg Leu Gln Asn Leu Glu His
 1 5 10 15
 Tyr Arg Phe Ala Lys Asn Val Leu Thr Leu Cys Arg Thr Ala Asn Ile
 20 25 30
 Ala Lys Leu Asn Pro Lys Leu Pro Glu Leu Glu Lys Ala Ile Glu Met
 35 40 45
 Glu Asp Leu Ala Leu Asn Pro Pro Val Ala Asn Glu Leu Thr Pro Gln
 50 55 60
 Val Ile Ala Leu Asp Glu Glu Arg Asp Arg Ala Tyr Gln Ala Leu Met
 65 70 75 80
 Ser Arg Val Arg Ser Tyr Ala Phe Asp Glu Asp Ser Gln Leu Arg Asn
 85 90 95
 Ala Ala Ala Arg Ile Glu Asp Val Ala Ala Arg Tyr Gly Asn Val Ile
 100 105 110

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Arg Met Asn Tyr Asp Lys Glu Thr Ala Ala Ile Glu Asn Phe Leu Thr
 115 120 125
 Asp Leu Lys Gly Glu Asn Ile Arg Pro Leu Val Thr Lys Leu Gly Val
 130 135 140
 Thr Ala Leu Val Asp Arg Leu Glu Lys Asn Asn Lys Ala Phe Ala Asp
 145 150 155 160
 Phe Phe Leu Arg Arg Leu Ser Thr Asp Gln Arg Gly Lys Tyr Asp Val
 165 170 175
 Lys Ala Leu Arg Ala Glu Thr Asp Arg Thr Leu Val Ala Val Val Arg
 180 185 190
 Arg Met Asp Ser Ile Asp Asp Met Glu Pro Ser Pro Glu Ile Arg Ala
 195 200 205
 Leu Ile Glu Leu Tyr Asn Arg Leu Val Ala Asn Arg Arg Ala Leu Leu
 210 215 220
 Ala Arg Arg Ala Ser Tyr Gly Glu Ala Ala Val Glu Lys Arg Arg Ala
 225 230 235 240
 Glu Ile Ala Glu Met Leu Arg Pro Leu Leu Ala Arg Ile Val Glu Glu
 245 250 255
 Lys Lys Thr Ala Val Phe Ala Gly Arg Thr Leu Gly Thr Gly Lys Asn
 260 265 270
 Arg His Tyr Leu Ile Thr Phe Val Ala Glu Asn Gly Asp Glu Glu Asp
 275 280 285
 Arg Trp Tyr Arg Ile Asn Gly Glu Gln Leu Val Tyr Val Pro Glu Asp
 290 295 300
 Glu Leu Pro Lys Pro Lys Lys Lys Lys Lys Pro Ala Ser Ser Thr Asp
 305 310 315 320
 Thr Pro Ser Glu Pro Pro Val Leu Pro Asp Pro Ser Gln Gly Gly Ser
 325 330 335
 Ser Ser Gly Gly Gly Glu Gln Gly Ser Thr Gly Gly Gly Leu
 340 345 350

(2) INFORMATION FOR SEQ ID NO:7:

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 87..3347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCAAGAATCA GGCCTTCTTA ATAACCAATT CAGGCCTTCC TCCGGGTTCT TACCGTAAAC	60
TAATTTACTA AAAGTTGGAG TTTTGT ATG GGA ACA GTT GTT GCT GAT CCC ACC	113
Met Gly Thr Val Val Ala Asp Pro Thr	
1 5	
GTT GCT GCG CCT GTG AAA ATG GCT AAA CAG ATA GCC GAA AAT GGT AAT	161
Val Ala Ala Pro Val Lys Met Ala Lys Gln Ile Ala Glu Asn Gly Asn	
10 15 20 25	
TAT GAT GTA GTG ATG ACT CGC TCT AAC TAT CTT CCT GTG ATC AAC CAA	209
Tyr Asp Val Val Met Thr Arg Ser Asn Tyr Leu Pro Val Ile Asn Gln	
30 35 40	
ATT CAG GCA GGA GAG CCT AGC CCC TAC CAG CCT GTT AAC AAC TTG ACT	257
Ile Gln Ala Gly Glu Pro Ser Pro Tyr Gln Pro Val Asn Asn Leu Thr	
45 50 55	
GCT CCA CCG GAG GGT GAG GAA GTG GCG CTC AAG TGG GAT ACC CCG AGC	305
Ala Pro Pro Glu Gly Glu Glu Val Ala Leu Lys Trp Asp Thr Pro Ser	
60 65 70	
GCA AAG AAG GCA GAA GCT TCC CGT GAA GTA AAA CGG ATC GGA GAC GGT	353
Ala Lys Lys Ala Glu Ala Ser Arg Glu Val Lys Arg Ile Gly Asp Gly	
75 80 85	
CTT TTC GTT ACG ATC GAA CCT GCA AAC GAT GTA CGT GCC AAC GAA GCC	401
Leu Phe Val Thr Ile Glu Pro Ala Asn Asp Val Arg Ala Asn Glu Ala	
90 95 100 105	
AAG GTT GTG CTC GCA GCA GAC AAC GTA TGG GGA GAC AAT ACG GGT TAC	449
Lys Val Val Leu Ala Ala Asp Asn Val Trp Gly Asp Asn Thr Gly Tyr	
110 115 120	
CAG TTC TTG TTG GAT GCC GAT CAC AAT ACA TTC GGA AGT GTC ATT CCG	497
Gln Phe Leu Leu Asp Ala Asp His Asn Thr Phe Gly Ser Val Ile Pro	
125 130 135	
GCA ACC GGT CCT CTC TTT ACC GGA ACA GCT TCT TCC AAT CTT TAC AGT	545
Ala Thr Gly Pro Leu Phe Thr Gly Thr Ala Ser Ser Asn Leu Tyr Ser	
140 145 150	
GCG AAC TTC GAG TAT TTG ATC CCG GCC AAT GCC GAT CCT GTT GTT ACT	593
Ala Asn Phe Glu Tyr Leu Ile Pro Ala Asn Ala Asp Pro Val Val Thr	
155 160 165	
ACA CAG AAT ATT ATC GTT ACA GGA CAG GGT GAA GTT GTA ATC CCC GGT	641
Thr Gln Asn Ile Ile Val Thr Gly Gln Gly Glu Val Val Ile Pro Gly	
170 175 180 185	
GGT GTT TAC GAC TAT TGC ATT ACG AAC CCG GAA CCT GCA TCC GGA AAG	689
Gly Val Tyr Asp Tyr Cys Ile Thr Asn Pro Glu Pro Ala Ser Gly Lys	
190 195 200	
ATG TGG ATC GCA GGA GAT GGA GAC AAC CAG CCT GCA CGT TAT GAC GAT	737
Met Trp Ile Ala Gly Asp Gly Asp Asn Gln Pro Ala Arg Tyr Asp Asp	
205 210 215	

TTC ACA TTC GAA GCA GGC AAG AAG TAC ACC TTC ACG ATG CGT CGC GCC Phe Thr Phe Glu Ala Gly Lys Lys Tyr Thr Phe Thr Met Arg Arg Ala 220 225 230	785
GGA ATG GGA GAT GGA ACT GAT ATG GAA GTC GAA GAC GAT TCA CCT GCA Gly Met Gly Asp Gly Thr Asp Met Glu Val Glu Asp Asp Ser Pro Ala 235 240 245	833
AGC TAT ACC TAT ACA GTC TAT CGT GAC GGC ACG AAG ATC AAG GAA GGT Ser Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Thr Lys Ile Lys Glu Gly 250 255 260 265	881
CTG ACG GCT ACG ACA TTC GAA GAA GAC GGT GTA GCT GCA GGC AAT CAT Leu Thr Ala Thr Thr Phe Glu Glu Asp Gly Val Ala Ala Gly Asn His 270 275 280	929
GAG TAT TGC GTG GAA GTT AAG TAC ACA GCC GGC GTA TCT CCG AAG GTA Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Val 285 290 295	977
TGT AAA GAC GTT ACG GTA GAA GGA TCC AAT GAA TTT GCT CCT GTA CAG Cys Lys Asp Val Thr Val Glu Gly Ser Asn Glu Phe Ala Pro Val Gln 300 305 310	1025
AAC CTG ACC GGT AGT GCA GTC GGC CAG AAA GTA ACG CTT AAG TGG GAT Asn Leu Thr Gly Ser Ala Val Gly Gln Lys Val Thr Leu Lys Trp Asp 315 320 325	1073
GCA CCT AAT GGT ACC CCA AAT CCG AAT CCG AAT CCG AAT CCG GGA ACA Ala Pro Asn Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn Pro Gly Thr 330 335 340 345	1121
ACA ACA CTT TCC GAA TCA TTC GAA AAT GGT ATT CCT GCC TCA TGG AAG Thr Thr Leu Ser Glu Ser Phe Glu Asn Gly Ile Pro Ala Ser Trp Lys 350 355 360	1169
ACG ATC GAT GCA GAC GGT GAC GGG CAT GGC TGG AAA CCT GGA AAT GCT Thr Ile Asp Ala Asp Gly Asp Gly His Gly Trp Lys Pro Gly Asn Ala 365 370 375	1217
CCC GGA ATC GCT GGC TAC AAT AGC AAT GGT TGT GTA TAT TCA GAG TCA Pro Gly Ile Ala Gly Tyr Asn Ser Asn Gly Cys Val Tyr Ser Glu Ser 380 385 390	1265
TTC GGT CTT GGT GGT ATA GGA GTT CTT ACC CCT GAC AAC TAT CTG ATA Phe Gly Leu Gly Gly Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Ile 395 400 405	1313
ACA CCG GCA TTG GAT TTG GCT AAC GGA GGT AAG TTG ACT TTC TGG GTA Thr Pro Ala Leu Asp Leu Ala Asn Gly Gly Lys Leu Thr Phe Trp Val 410 415 420 425	1361
TGC GCA CAG GAT GCT AAT TAT GCA TCC GAG CAC TAT GCG GTG TAT GCA Cys Ala Gln Asp Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr Ala 430 435 440	1409
TCT TCG ACC GGT AAC GAT GCA TCC AAC TTC ACG AAT GCT TTG TTG GAA Ser Ser Thr Gly Asn Asp Ala Ser Asn Phe Thr Asn Ala Leu Leu Glu 445 450 455	1457
GAG ACG ATT ACG GCA AAA GGT GTT CGC TCG CCG GAA GCT ATT CGT GGT Glu Thr Ile Thr Ala Lys Gly Val Arg Ser Pro Glu Ala Ile Arg Gly 460 465 470	1505

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CGT	ATA	CAG	GGT	ACT	TGG	CGC	CAG	AAG	ACG	GTA	GAC	CTT	CCC	GCA	GGT	1553
Arg	Ile	Gln	Gly	Thr	Trp	Arg	Gln	Lys	Thr	Val	Asp	Leu	Pro	Ala	Gly	
	475						480				485					
ACG	AAA	TAT	GTT	GCT	TTC	CGT	CAC	TTC	CAA	AGC	ACG	GAT	ATG	TTC	TAC	1601
Thr	Lys	Tyr	Val	Ala	Phe	Arg	His	Phe	Gln	Ser	Thr	Asp	Met	Phe	Tyr	
	490				495					500					505	
ATC	GAC	CTT	GAT	GAG	GTT	GAG	ATC	AAG	GCC	AAT	GGC	AAG	CGC	GCA	GAC	1649
Ile	Asp	Leu	Asp	Glu	Val	Glu	Ile	Lys	Ala	Asn	Gly	Lys	Arg	Ala	Asp	
				510					515					520		
TTC	ACG	GAA	ACG	TTC	GAG	TCT	TCT	ACT	CAT	GGA	GAG	GCA	CCA	GCG	GAA	1697
Phe	Thr	Glu	Thr	Phe	Glu	Ser	Ser	Thr	His	Gly	Glu	Ala	Pro	Ala	Glu	
			525					530					535			
TGG	ACT	ACT	ATC	GAT	GCC	GAT	GGC	GAT	GGT	CAG	GAT	TGG	CTC	TGT	CTG	1745
Trp	Thr	Thr	Ile	Asp	Ala	Asp	Gly	Asp	Gly	Gln	Asp	Trp	Leu	Cys	Leu	
		540					545					550				
TCT	TCC	GGA	CAA	TTG	GAC	TGG	CTG	ACA	GCT	CAT	GGC	GGC	ACC	AAC	GTA	1793
Ser	Ser	Gly	Gln	Leu	Asp	Trp	Leu	Thr	Ala	His	Gly	Gly	Thr	Asn	Val	
	555					560					565					
GTA	GCC	TCT	TTC	TCA	TGG	AAT	GGA	ATG	GCT	TTG	AAT	CCT	GAT	AAC	TAT	1841
Val	Ala	Ser	Phe	Ser	Trp	Asn	Gly	Met	Ala	Leu	Asn	Pro	Asp	Asn	Tyr	
	570				575					580					585	
CTC	ATC	TCA	AAG	GAT	GTT	ACA	GGC	GCA	ACG	AAG	GTA	AAG	TAC	TAC	TAT	1889
Leu	Ile	Ser	Lys	Asp	Val	Thr	Gly	Ala	Thr	Lys	Val	Lys	Tyr	Tyr	Tyr	
			590						595					600		
GCA	GTC	AAC	GAC	GGT	TTT	CCC	GGG	GAT	CAC	TAT	GCG	GTG	ATG	ATC	TCC	1937
Ala	Val	Asn	Asp	Gly	Phe	Pro	Gly	Asp	His	Tyr	Ala	Val	Met	Ile	Ser	
			605					610					615			
AAG	ACG	GGC	ACG	AAC	GCC	GGA	GAC	TTC	ACG	GTT	GTT	TTC	GAA	GAA	ACG	1985
Lys	Thr	Gly	Thr	Asn	Ala	Gly	Asp	Phe	Thr	Val	Val	Phe	Glu	Glu	Thr	
		620					625					630				
CCT	AAC	GGA	ATA	AAT	AAG	GGC	GGA	GCA	AGA	TTC	GGT	CTT	TCC	ACG	GAA	2033
Pro	Asn	Gly	Ile	Asn	Lys	Gly	Gly	Ala	Arg	Phe	Gly	Leu	Ser	Thr	Glu	
	635					640					645					
GCC	AAT	GGC	GCC	AAA	CCT	CAA	AGT	GTA	TGG	ATC	GAG	CGT	ACG	GTA	GAT	2081
Ala	Asn	Gly	Ala	Lys	Pro	Gln	Ser	Val	Trp	Ile	Glu	Arg	Thr	Val	Asp	
	650				655					660					665	
TTG	CCT	GCG	GGC	ACG	AAG	TAT	GTT	GCT	TTC	CGT	CAC	TAC	AAT	TGC	TCG	2129
Leu	Pro	Ala	Gly	Thr	Lys	Tyr	Val	Ala	Phe	Arg	His	Tyr	Asn	Cys	Ser	
			670						675					680		
GAT	TTG	GAC	TAC	ATT	CTT	TTG	GAT	GAT	ATT	CAG	TTC	ACC	ATG	GGT	GGC	2177
Asp	Leu	Asp	Tyr	Ile	Leu	Leu	Asp	Asp	Ile	Gln	Phe	Thr	Met	Gly	Gly	
			685					690					695			
AGC	CCC	ACC	CCG	ACC	GAT	TAT	ACC	TAC	ACG	GTA	TAT	CGT	GAT	GGT	ACG	2225
Ser	Pro	Thr	Pro	Thr	Asp	Tyr	Thr	Tyr	Thr	Val	Tyr	Arg	Asp	Gly	Thr	
		700					705					710				
AAG	ATC	AAG	GAA	GGT	CTG	ACC	GAA	ACG	ACC	TTC	GAA	GAA	GAC	GGC	GTA	2273
Lys	Ile	Lys	Glu	Gly	Leu	Thr	Glu	Thr	Thr	Phe	Glu	Glu	Asp	Gly	Val	
	715					720					725					

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GCT ACG GGC AAT CAT GAG TAT TGC GTG GAA GTG AAG TAC ACA GCC GGC Ala Thr Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly 730 735 740 745	2321
GTA TCT CCG AAG GTG TGT GTA AAC GTA ACT ATT AAT CCG ACT CAG TTC Val Ser Pro Lys Val Cys Val Asn Val Thr Ile Asn Pro Thr Gln Phe 750 755 760	2369
AAT CCT GTA AAG AAC CTG AAG GCA CAA CCG GAT GGC GGC GAC GTG GTT Asn Pro Val Lys Asn Leu Lys Ala Gln Pro Asp Gly Gly Asp Val Val 765 770 775	2417
CTC AAG TGG GAA GCC CCG AGT GGC AAA CGA GGA GAA CTG CTT AAT GAA Leu Lys Trp Glu Ala Pro Ser Gly Lys Arg Gly Glu Leu Leu Asn Glu 780 785 790	2465
GAT TTT GAA GGA GAC GCT ATT CCC ACA GGG TGG ACA GCA TTG GAT GCC Asp Phe Glu Gly Asp Ala Ile Pro Thr Gly Trp Thr Ala Leu Asp Ala 795 800 805	2513
GAT GGT GAC GGT AAT AAC TGG GAT ATC ACG CTC AAT GAA TTT ACG CGA Asp Gly Asp Gly Asn Asn Trp Asp Ile Thr Leu Asn Glu Phe Thr Arg 810 815 820 825	2561
GGA GAG CGT CAT GTT CTT TCA CCT TTA CGC GCC AGC AAC GTA GCC ATA Gly Glu Arg His Val Leu Ser Pro Leu Arg Ala Ser Asn Val Ala Ile 830 835 840	2609
TCC TAT TCT TCT TTA CTT CAG GGT CAA GAA TAT TTG CCT CTC ACG CCG Ser Tyr Ser Ser Leu Leu Gln Gly Gln Glu Tyr Leu Pro Leu Thr Pro 845 850 855	2657
AAC AAC TTT CTG ATC ACT CCG AAG GTT GAA GGA GCA AAG AAG ATT ACT Asn Asn Phe Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Lys Ile Thr 860 865 870	2705
TAT AAG GTG GGT TCA CCG GGT CTT CCT CAA TGG AGT CAT GAT CAT TAT Tyr Lys Val Gly Ser Pro Gly Leu Pro Gln Trp Ser His Asp His Tyr 875 880 885	2753
GCA CTC TGT ATC TCC AAG AGC GGA ACG GCT GCA GCC GAC TTC GAA GTA Ala Leu Cys Ile Ser Lys Ser Gly Thr Ala Ala Ala Asp Phe Glu Val 890 895 900 905	2801
ATC TTT GAA GAA ACG ATG ACC TAC ACT CAA GGA GGA GCC AAC TTG ACA Ile Phe Glu Glu Thr Met Thr Tyr Thr Gln Gly Gly Ala Asn Leu Thr 910 915 920	2849
AGA GAA AAA GAC CTC CCT GCC GGC ACG AAA TAT GTC GCT TTC CGT CAT Arg Glu Lys Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His 925 930 935	2897
TAC AAT TGC ACG GAT GTT CTG GGC ATA ATG ATT GAC GAT GTA GTG ATA Tyr Asn Cys Thr Asp Val Leu Gly Ile Met Ile Asp Asp Val Val Ile 940 945 950	2945
ACA GGT GAA GGC GAA GGT CCC AGT TAC ACC TAC ACG GTG TAT CGT GAC Thr Gly Glu Gly Glu Gly Pro Ser Tyr Thr Tyr Thr Val Tyr Arg Asp 955 960 965	2993
GGC ACG AAG ATC CAG GAA GGT CTG ACC GAA ACG ACC TAC CGC GAT GCA Gly Thr Lys Ile Gln Glu Gly Leu Thr Glu Thr Thr Tyr Arg Asp Ala 970 975 980 985	3041

64

GGA ATG AGT GCA CAA TCT CAT GAG TAT TGC GTA GAG GTT AAG TAC GCA Gly Met Ser Ala Gln Ser His Glu Tyr Cys Val Glu Val Lys Tyr Ala 990 995 1000	3089
GCC GGC GTA TCT CCG AAG GTT TGT GTG GAT TAT ATT CCT GAT GGA GTG Ala Gly Val Ser Pro Lys Val Cys Val Asp Tyr Ile Pro Asp Gly Val 1005 1010 1015	3137
GCA GAC GTA ACT GCT CAG AAG CCT TAC ACG CTG ACG GTT GTA GGA AAG Ala Asp Val Thr Ala Gln Lys Pro Tyr Thr Leu Thr Val Val Gly Lys 1020 1025 1030	3185
ACT ATC ACG GTA ACT TGC CAA GGC GAA GCT ATG ATC TAC GAC ATG AAC Thr Ile Thr Val Thr Cys Gln Gly Glu Ala Met Ile Tyr Asp Met Asn 1035 1040 1045	3233
GGT CGT CGT CTG GCA GCG GGT CGC AAC ACG GTT GTT TAC ACG GCT CAG Gly Arg Arg Leu Ala Ala Gly Arg Asn Thr Val Val Tyr Thr Ala Gln 1050 1055 1060 1065	3281
GGC GGC TAC TAT GCA GTC ATG GTT GTC GTT GAC GGC AAG TCT TAC GTA Gly Gly Tyr Tyr Ala Val Met Val Val Asp Gly Lys Ser Tyr Val 1070 1075 1080	3329
GAG AAA CTC GCT ATC AAG TAATTCTGTC TTGGACTCGG AGACTTTGTG Glu Lys Leu Ala Ile Lys 1085	3377
CAGACACTTT TAATATAGGT CTGTAATTGT CTCAGAGTAT GAATCGGTCTG CCCGACTTCC	3437
TTAAAAGGAG GTCGGGCGAC TTCGTTTTTA TTATTGCTGT CTGGTAAACT TGTCAGAGG	3497
AGACCTTTGA AAAATGGGGC GGTCAATAAT TTTCGGTCTA TGGGTCAAAT TGCAGGCTAC	3557
TGTTTTAGGT GTATGTTGGG CTATCTTCCT ATCTTTAAGA GACCTTTGAA AAATAAGGAG	3617
ATGGAGGGAA GAGGAGTTCT TGGCATAAAA GGAGCGAGTG AAAGGGGTGG CAGTAAGGAG	3677
TGAAAGTAGT TGTAATCCC CCCTTTGAGG AGCTACTTGT ACGAGCTCCT CAAGGGTGGT	3737
TATGCCTTAT CCTACGGATG AGGACATAAT TATCCCCGGC GTTCTGTATA AATTAAAGGC	3797
GATGCTTTCA AGAATGTTTT GAGTATGGGT CTGGCAAGT CCCCAGTATC GACATGTCCG	3857
CCATGAAACC ACCGGCGAAT ACTGCCAAG GTGCGTTCGA TGGTGCTCCG TATCGGACTG	3917
ATTGCTTTGT TTCGTTGCTT CTCTTCCTCG GTCATGCCC TGTTCGTTG TGCCTTGTGC	3977
ATAATGCCGT CTTGAAGGTG ATGGGTTTGC AGGTAGGAAC GATTTTCCCC GCAAGCATAT	4037
CCTTTGTCCG CCAAGACGGC TGTACCTTGA GGTATGTTTG CAC	4080

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1087 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

65

M t Gly Thr Val Val Ala Asp Pro Thr Val Ala Ala Pro Val Lys Met
1 5 10 15
Ala Lys Gln Ile Ala Glu Asn Gly Asn Tyr Asp Val Val Met Thr Arg
20 25 30
Ser Asn Tyr Leu Pro Val Ile Asn Gln Ile Gln Ala Gly Glu Pro Ser
35 40 45
Pro Tyr Gln Pro Val Asn Asn Leu Thr Ala Pro Pro Glu Gly Glu Glu
50 55 60
Val Ala Leu Lys Trp Asp Thr Pro Ser Ala Lys Lys Ala Glu Ala Ser
65 70 75 80
Arg Glu Val Lys Arg Ile Gly Asp Gly Leu Phe Val Thr Ile Glu Pro
85 90 95
Ala Asn Asp Val Arg Ala Asn Glu Ala Lys Val Val Leu Ala Ala Asp
100 105 110
Asn Val Trp Gly Asp Asn Thr Gly Tyr Gln Phe Leu Leu Asp Ala Asp
115 120 125
His Asn Thr Phe Gly Ser Val Ile Pro Ala Thr Gly Pro Leu Phe Thr
130 135 140
Gly Thr Ala Ser Ser Asn Leu Tyr Ser Ala Asn Phe Glu Tyr Leu Ile
145 150 155 160
Pro Ala Asn Ala Asp Pro Val Val Thr Thr Gln Asn Ile Ile Val Thr
165 170 175
Gly Gln Gly Glu Val Val Ile Pro Gly Gly Val Tyr Asp Tyr Cys Ile
180 185 190
Thr Asn Pro Glu Pro Ala Ser Gly Lys Met Trp Ile Ala Gly Asp Gly
195 200 205
Asp Asn Gln Pro Ala Arg Tyr Asp Asp Phe Thr Phe Glu Ala Gly Lys
210 215 220
Lys Tyr Thr Phe Thr Met Arg Arg Ala Gly Met Gly Asp Gly Thr Asp
225 230 235 240
Met Glu Val Glu Asp Asp Ser Pro Ala Ser Tyr Thr Tyr Thr Val Tyr
245 250 255
Arg Asp Gly Thr Lys Ile Lys Glu Gly Leu Thr Ala Thr Thr Phe Glu
260 265 270
Glu Asp Gly Val Ala Ala Gly Asn His Glu Tyr Cys Val Glu Val Lys
275 280 285
Tyr Thr Ala Gly Val Ser Pro Lys Val Cys Lys Asp Val Thr Val Glu
290 295 300
Gly Ser Asn Glu Phe Ala Pro Val Gln Asn Leu Thr Gly Ser Ala Val
305 310 315 320
Gly Gln Lys Val Thr Leu Lys Trp Asp Ala Pro Asn Gly Thr Pro Asn
325 330 335

Pro	Asn	Pro	Asn	Pro	Asn	Pro	Gly	Thr	Thr	Leu	Ser	Glu	Ser	Phe	
			340					345					350		
Glu	Asn	Gly	Ile	Pro	Ala	Ser	Trp	Lys	Thr	Ile	Asp	Ala	Asp	Gly	Asp
		355					360				365				
Gly	His	Gly	Trp	Lys	Pro	Gly	Asn	Ala	Pro	Gly	Ile	Ala	Gly	Tyr	Asn
	370					375					380				
Ser	Asn	Gly	Cys	Val	Tyr	Ser	Glu	Ser	Phe	Gly	Leu	Gly	Gly	Ile	Gly
385					390					395					400
Val	Leu	Thr	Pro	Asp	Asn	Tyr	Leu	Ile	Thr	Pro	Ala	Leu	Asp	Leu	Ala
				405					410					415	
Asn	Gly	Gly	Lys	Leu	Thr	Phe	Trp	Val	Cys	Ala	Gln	Asp	Ala	Asn	Tyr
			420					425					430		
Ala	Ser	Glu	His	Tyr	Ala	Val	Tyr	Ala	Ser	Ser	Thr	Gly	Asn	Asp	Ala
		435					440					445			
Ser	Asn	Phe	Thr	Asn	Ala	Leu	Leu	Glu	Glu	Thr	Ile	Thr	Ala	Lys	Gly
	450					455					460				
Val	Arg	Ser	Pro	Glu	Ala	Ile	Arg	Gly	Arg	Ile	Gln	Gly	Thr	Trp	Arg
465					470					475					480
Gln	Lys	Thr	Val	Asp	Leu	Pro	Ala	Gly	Thr	Lys	Tyr	Val	Ala	Phe	Arg
				485					490					495	
His	Phe	Gln	Ser	Thr	Asp	Met	Phe	Tyr	Ile	Asp	Leu	Asp	Glu	Val	Glu
			500					505					510		
Ile	Lys	Ala	Asn	Gly	Lys	Arg	Ala	Asp	Phe	Thr	Glu	Thr	Phe	Glu	Ser
		515					520					525			
Ser	Thr	His	Gly	Glu	Ala	Pro	Ala	Glu	Trp	Thr	Thr	Ile	Asp	Ala	Asp
	530					535					540				
Gly	Asp	Gly	Gln	Asp	Trp	Leu	Cys	Leu	Ser	Ser	Gly	Gln	Leu	Asp	Trp
545					550					555					560
Leu	Thr	Ala	His	Gly	Gly	Thr	Asn	Val	Val	Ala	Ser	Phe	Ser	Trp	Asn
				565					570					575	
Gly	Met	Ala	Leu	Asn	Pro	Asp	Asn	Tyr	Leu	Ile	Ser	Lys	Asp	Val	Thr
			580					585					590		
Gly	Ala	Thr	Lys	Val	Lys	Tyr	Tyr	Tyr	Ala	Val	Asn	Asp	Gly	Phe	Pro
		595					600					605			
Gly	Asp	His	Tyr	Ala	Val	Met	Ile	Ser	Lys	Thr	Gly	Thr	Asn	Ala	Gly
	610					615					620				
Asp	Phe	Thr	Val	Val	Phe	Glu	Glu	Thr	Pro	Asn	Gly	Ile	Asn	Lys	Gly
625					630					635					640
Gly	Ala	Arg	Phe	Gly	Leu	Ser	Thr	Glu	Ala	Asn	Gly	Ala	Lys	Pro	Gln
				645					650					655	
Ser	Val	Trp	Ile	Glu	Arg	Thr	Val	Asp	Leu	Pro	Ala	Gly	Thr	Lys	Tyr
			660					665					670		

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Val Ala Phe Arg His Tyr Asn Cys Ser Asp Leu Asp Tyr Il Leu Leu
 675 680 685
 Asp Asp Ile Gln Phe Thr Met Gly Gly Ser Pro Thr Pro Thr Asp Tyr
 690 695 700
 Thr Tyr Thr Val Tyr Arg Asp Gly Thr Lys Ile Lys Glu Gly Leu Thr
 705 710 715 720
 Glu Thr Thr Phe Glu Asp Gly Val Ala Thr Gly Asn His Glu Tyr
 725 730 735
 Cys Val Glu Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Val Cys Val
 740 745 750
 Asn Val Thr Ile Asn Pro Thr Gln Phe Asn Pro Val Lys Asn Leu Lys
 755 760 765
 Ala Gln Pro Asp Gly Gly Asp Val Val Leu Lys Trp Glu Ala Pro Ser
 770 775 780
 Gly Lys Arg Gly Glu Leu Leu Asn Glu Asp Phe Glu Gly Asp Ala Ile
 785 790 795 800
 Pro Thr Gly Trp Thr Ala Leu Asp Ala Asp Gly Asp Gly Asn Asn Trp
 805 810 815
 Asp Ile Thr Leu Asn Glu Phe Thr Arg Gly Glu Arg His Val Leu Ser
 820 825 830
 Pro Leu Arg Ala Ser Asn Val Ala Ile Ser Tyr Ser Ser Leu Leu Gln
 835 840 845
 Gly Gln Glu Tyr Leu Pro Leu Thr Pro Asn Asn Phe Leu Ile Thr Pro
 850 855 860
 Lys Val Glu Gly Ala Lys Lys Ile Thr Tyr Lys Val Gly Ser Pro Gly
 865 870 875 880
 Leu Pro Gln Trp Ser His Asp His Tyr Ala Leu Cys Ile Ser Lys Ser
 885 890 895
 Gly Thr Ala Ala Ala Asp Phe Glu Val Ile Phe Glu Glu Thr Met Thr
 900 905 910
 Tyr Thr Gln Gly Gly Ala Asn Leu Thr Arg Glu Lys Asp Leu Pro Ala
 915 920 925
 Gly Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys Thr Asp Val Leu
 930 935 940
 Gly Ile Met Ile Asp Asp Val Val Ile Thr Gly Glu Gly Glu Gly Pro
 945 950 955 960
 Ser Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Thr Lys Ile Gln Glu Gly
 965 970 975
 Leu Thr Glu Thr Thr Tyr Arg Asp Ala Gly Met Ser Ala Gln Ser His
 980 985 990
 Glu Tyr Cys Val Glu Val Lys Tyr Ala Ala Gly Val Ser Pro Lys Val
 995 1000 1005

68

Cys Val Asp Tyr Ile Pr Asp Gly Val Ala Asp Val Thr Ala Gln Lys
 1010 1015 1020

Pro Tyr Thr Leu Thr Val Val Gly Lys Thr Ile Thr Val Thr Cys Gln
 1025 1030 1035 1040

Gly Glu Ala Met Ile Tyr Asp Met Asn Gly Arg Arg Leu Ala Ala Gly
 1045 1050 1055

Arg Asn Thr Val Val Tyr Thr Ala Gln Gly Gly Tyr Tyr Ala Val Met
 1060 1065 1070

Val Val Val Asp Gly Lys Ser Tyr Val Glu Lys Leu Ala Ile Lys
 1075 1080 1085

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6895 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 696..5894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGATCCTACG CCCGATACCC ATACTCGAAG CCTTTGCTCA GTACCATCCT GCAGAAGGTT 60

ACTCTTTTCGC ATATAGTGAC CCTCTTTTCT CTCAGCATAA TGGTACCTAT CATATCAGTA 120

AGGGGCGTAT TGTCTTTTCG AACAAATGTAC AGCCCCGAGAA CTCTTTACTT CCACATCACA 180

CCCCCGACTC CTTAGTCAAG GATCTTTTTT CCCCTTTCCC CTCCGCTCTC TTCCTCATGC 240

TGGACTGACT TAACCTTGGT CTGCTCTACT TTTCGTTGT AAATACATGC AACACRATAA 300

CTTTAAGTGT TGTTAGACAA CACTTTTACA AGACTCTGAC TTTTAATGAG GTGGAGCATG 360

AACCTTTTCC TCTTTCATCT TCTCCTTCAG ATTACAGTCA ATATTTTGGC AAAAGGCTAA 420

TTGACAGCCT TTTATAAGGG TTAATCCCTT GTGGCTTATA TTGAAAACAT GTTCTTTATA 480

ATCCGATACT CTTCTTAAAT CGAATTTTTT CTCTAAATTG CGCCGCAACA AAACCTCTTG 540

AGAAAAGTAC CAATAGAAAT AGAAGGTAGC ATTTTGCCCT TAAATTCCTT TTCTTTTCTT 600

GGATTGTTCT TGAATGAAT CTTATTTGTG GATTTTTTTT GTTTTTTTAA CCCGGCCGTG 660

GTTCTCTGAA TCACGACCAT AAATTGTTTT AAAGT ATG AGG AAA TTA TTA TTG 713
 Met Arg Lys Leu Leu
 1 5

CTG ATC GCG GCG TCC CTT TTG GGA GTT GGT CTT TAC GCC CAA AGC GCC 761
 Leu Ile Ala Ala Ser Leu Leu Gly Val Gly Leu Tyr Ala Gln Ser Ala
 10 15 20

AAG ATT AAG CTT GAT GCT CCG ACT ACT CGA ACG ACA TGT ACG AAC AAT Lys Ile Lys Leu Asp Ala Pro Thr Thr Arg Thr Thr Cys Thr Asn Asn 25 30 35	809
AGC TTC AAG CAG TTC GAT GCA AGC TTT TCG TTC AAT GAA GTC GAG CTG Ser Phe Lys Gln Phe Asp Ala Ser Phe Ser Phe Asn Glu Val Glu Leu 40 45 50	857
ACA AAG GTG GAG ACC AAA GGT GGT ACT TTC GCC TCA GTG TCA ATT CCG Thr Lys Val Glu Thr Lys Gly Gly Thr Phe Ala Ser Val Ser Ile Pro 55 60 65 70	905
GGT GCA TTC CCG ACC GGT GAG GTT GGT TCT CCC GAA GTG CCA GCA GTT Gly Ala Phe Pro Thr Gly Glu Val Gly Ser Pro Glu Val Pro Ala Val 75 80 85	953
AGG AAG TTG ATT GCT GTG CCT GTC GGA GCC ACA CCT GTT GTT CGC GTG Arg Lys Leu Ile Ala Val Pro Val Gly Ala Thr Pro Val Val Arg Val 90 95 100	1001
AAA AGT TTT ACC GAG CAA GTT TAC TCT CTG AAC CAA TAC GGT TCC GAA Lys Ser Phe Thr Glu Gln Val Tyr Ser Leu Asn Gln Tyr Gly Ser Glu 105 110 115	1049
AAA CTC ATG CCA CAT CAA CCC TCT ATG AGC AAG AGT GAT GAT CCC GAA Lys Leu Met Pro His Gln Pro Ser Met Ser Lys Ser Asp Asp Pro Glu 120 125 130	1097
AAG GTT CCC TTC GTT TAC AAT GCT GCT GCT TAT GCA CGC AAA GGT TTT Lys Val Pro Phe Val Tyr Asn Ala Ala Tyr Ala Arg Lys Gly Phe 135 140 145 150	1145
GTC GGA CAA GAA CTG ACC CAA GTA GAA ATG TTG GGG ACA ATG CGT GGT Val Gly Gln Glu Leu Thr Gln Val Glu Met Leu Gly Thr Met Arg Gly 155 160 165	1193
GTT CGC ATT GCA GCT CTT ACC ATT AAT CCT GTT CAG TAT GAT GTG GTT Val Arg Ile Ala Ala Leu Thr Ile Asn Pro Val Gln Tyr Asp Val Val 170 175 180	1241
GCA AAC CAA TTG AAG GTT AGA AAC AAC ATC GAA ATT GAA GTA AGC TTT Ala Asn Gln Leu Lys Val Arg Asn Asn Ile Glu Ile Glu Val Ser Phe 185 190 195	1289
CAA GGA GCT GAT GAA GTA GCT ACA CAA CGT TTG TAT GAT GCT TCT TTT Gln Gly Ala Asp Glu Val Ala Thr Gln Arg Leu Tyr Asp Ala Ser Phe 200 205 210	1337
AGC CCT TAT TTC GAA ACA GCT TAT AAA CAG CTC TTC AAT AGA GAT GTT Ser Pro Tyr Phe Glu Thr Ala Tyr Lys Gln Phe Asn Arg Asp Val 215 220 225 230	1385
TAT ACA GAT CAT GGC GAC TTG TAT AAT ACG CCG GTT CGT ATG CTT GTT Tyr Thr Asp His Gly Asp Leu Tyr Asn Thr Pro Val Arg Met Leu Val 235 240 245	1433
GTT GCA GGT GCA AAA TTC AAA GAA GCT CTC AAG CCT TGG CTC ACT TGG Val Ala Gly Ala Lys Phe Lys Glu Ala Leu Lys Pro Trp Leu Thr Trp 250 255 260	1481
AAG GCT CAA AAG GGC TTC TAT CTG GAT GTG CAT TAC ACA GAC GAA GCT Lys Ala Gln Lys Gly Phe Tyr Leu Asp Val His Tyr Thr Asp Glu Ala 265 270 275	1529

70

GAA GTA GGA ACG ACA AAC GCC TCT ATC AAG GCA TTT ATT CAC AAG AAA Glu Val Gly Thr Thr Asn Ala Ser Ile Lys Ala Phe Ile His Lys Lys 280 285 290	1577
TAC AAT GAT GGA TTG GCA GCT AGT GCT GCT CCG GTC TTC TTG GCT TTG Tyr Asn Asp Gly Leu Ala Ala Ser Ala Ala Pro Val Phe Leu Ala Leu 295 300 305 310	1625
GTT GGT GAC ACT GAC GTT ATT AGC GGA GAA AAA GGA AAG AAA ACA AAA Val Gly Asp Thr Asp Val Ile Ser Gly Glu Lys Gly Lys Lys Thr Lys 315 320 325	1673
AAA GTT ACC GAC TTG TAT TAC AGT GCA GTC GAT GGC GAC TAT TTC CCT Lys Val Thr Asp Leu Tyr Tyr Ser Ala Val Asp Gly Asp Tyr Phe Pro 330 335 340	1721
GAA ATG TAT ACT TTC CGT ATG TCT GCT TCT TCC CCA GAA GAA CTG ACG Glu Met Tyr Thr Phe Arg Met Ser Ala Ser Ser Pro Glu Leu Thr 345 350 355	1769
AAC ATC ATT GAT AAG GTA TTG ATG TAT GAA AAG GCT ACT ATG CCA GAT Asn Ile Ile Asp Lys Val Leu Met Tyr Glu Lys Ala Thr Met Pro Asp 360 365 370	1817
AAG AGT TAT TTG GAG AAA GTT CTC TTG ATT GCA GGT GCA GAT TAT AGC Lys Ser Tyr Leu Glu Lys Val Leu Leu Ile Ala Gly Ala Asp Tyr Ser 375 380 385 390	1865
TGG AAT TCC CAG GTA GGT CAG CCA ACC ATT AAA TAC GGT ATG CAG TAC Trp Asn Ser Gln Val Gly Gln Pro Thr Ile Lys Tyr Gly Met Gln Tyr 395 400 405	1913
TAC TAC AAC CAA GAG CAT GGT TAT ACC GAC GTG TAC AAC TAT CTC AAA Tyr Tyr Asn Gln Glu His Gly Tyr Thr Asp Val Tyr Asn Tyr Leu Lys 410 415 420	1961
GCC CCT TAT ACA GGT TGC TAC AGT CAT TTG AAT ACC GGA GTC AGC TTT Ala Pro Tyr Thr Gly Cys Tyr Ser His Leu Asn Thr Gly Val Ser Phe 425 430 435	2009
GCA AAC TAT ACA GCG CAT GGA TCT GAG ACC GCA TGG GCT GAT CCA CTT Ala Asn Tyr Thr Ala His Gly Ser Glu Thr Ala Trp Ala Asp Pro Leu 440 445 450	2057
CTG ACT ACT TCT CAA CTG AAA GCA CTC ACT AAT AAG GAC AAA TAC TTC Leu Thr Thr Ser Gln Leu Lys Ala Leu Thr Asn Lys Asp Lys Tyr Phe 455 460 465 470	2105
TTA GCT ATT GGC AAC TGC TGT ATT ACA GCT CAA TTC GAT TAT GTA CAG Leu Ala Ile Gly Asn Cys Cys Ile Thr Ala Gln Phe Asp Tyr Val Gln 475 480 485	2153
CCT TGC TTC GGA GAG GTA ATA ACT CGC GTT AAG GAG AAA GGG GCT TAT Pro Cys Phe Gly Glu Val Ile Thr Arg Val Lys Glu Lys Gly Ala Tyr 490 495 500	2201
GCC TAT ATC GGT TCA TCT CCA AAT TCT TAT TGG GGC GAG GAC TAC TAT Ala Tyr Ile Gly Ser Ser Pro Asn Ser Tyr Trp Gly Glu Asp Tyr Tyr 505 510 515	2249

TGG AGT GTG GGT GCT AAT GCC GTA TTT GGT GTT CAG CCT ACT TTT GAA	2297
Trp Ser Val Gly Ala Asn Ala Val Phe Gly Val Gln Pro Thr Phe Glu	
520 525 530	
GGT ACG TCT ATG GGT TCT TAT GAT GCT ACA TTC TTG GAG GAT TCG TAC	2345
Gly Thr Ser Met Gly Ser Tyr Asp Ala Thr Phe Leu Glu Asp Ser Tyr	
535 540 545 550	
AAC ACA GTG AAT TCT ATT ATG TGG GCA GGT AAT CTT GCC GCT ACT CAT	2393
Asn Thr Val Asn Ser Ile Met Trp Ala Gly Asn Leu Ala Ala Thr His	
555 560 565	
GCT GGA AAT ATC GGC AAT ATT ACC CAT ATT GGT GCT CAT TAC TAT TGG	2441
Ala Gly Asn Ile Gly Asn Ile Thr His Ile Gly Ala His Tyr Tyr Trp	
570 575 580	
GAA GCT TAT CAT GTC CTT GGC GAT GGT TCG GTT ATG CCT TAT CGT GCA	2489
Glu Ala Tyr His Val Leu Gly Asp Gly Ser Val Met Pro Tyr Arg Ala	
585 590 595	
ATG CCT AAG ACC AAT ACT TAT ACG CTT CCT GCC TCT TTG CCT CAG AAT	2537
Met Pro Lys Thr Asn Thr Tyr Thr Leu Pro Ala Ser Leu Pro Gln Asn	
600 605 610	
CAG GCT TCT TAT AGC ATT CAG GCT TCT GCC GGT TCT TAC GTA GCT ATT	2585
Gln Ala Ser Tyr Ser Ile Gln Ala Ser Ala Gly Ser Tyr Val Ala Ile	
615 620 625 630	
TCT AAA GAT GGA GTT TTG TAT GGA ACA GGT GTT GCT AAT GCC AGC GGT	2633
Ser Lys Asp Gly Val Leu Tyr Gly Thr Gly Val Ala Asn Ala Ser Gly	
635 640 645	
GTT GCG ACT GTG AGT ATG ACT AAG CAG ATT ACG GAA AAT GGT AAT TAT	2681
Val Ala Thr Val Ser Met Thr Lys Gln Ile Thr Glu Asn Gly Asn Tyr	
650 655 660	
GAT GTA GTT ATC ACT CGC TCT AAT TAT CTT CCT GTG ATC AAG CAA ATT	2729
Asp Val Val Ile Thr Arg Ser Asn Tyr Leu Pro Val Ile Lys Gln Ile	
665 670 675	
CAG GTA GGT GAG CCT AGC CCC TAC CAG CCC GTT TCC AAC TTG ACA GCT	2777
Gln Val Gly Glu Pro Ser Pro Tyr Gln Pro Val Ser Asn Leu Thr Ala	
680 685 690	
ACA ACG CAG GGT CAG AAA GTA ACG CTC AAG TGG GAA GCA CCG AGC GCA	2825
Thr Thr Gln Gly Gln Lys Val Thr Leu Lys Trp Glu Ala Pro Ser Ala	
695 700 705 710	
AAG AAG GCA GAA GGT TCC CGT GAA GTA AAA CGG ATC GGA GAC GGT CTT	2873
Lys Lys Ala Glu Gly Ser Arg Glu Val Lys Arg Ile Gly Asp Gly Leu	
715 720 725	
TTC GTT ACG ATC GAA CCT GCA AAC GAT GTA CGT GCC AAC GAA GCC AAG	2921
Phe Val Thr Ile Glu Pro Ala Asn Asp Val Arg Ala Asn Glu Ala Lys	
730 735 740	
GTT GTG CTT GCG GCA GAC AAC GTA TGG GGA GAC AAT ACG GGT TAC CAG	2969
Val Val Leu Ala Ala Asp Asn Val Trp Gly Asp Asn Thr Gly Tyr Gln	
745 750 755	
TTC TTG TTG GAT GCC GAT CAC AAT ACA TTC GGA AGT GTC ATT CCG GCA	3017
Phe Leu Leu Asp Ala Asp His Asn Thr Phe Gly Ser Val Ile Pro Ala	
760 765 770	

ACC GGT CCT CTC TTT ACC GGA ACA GCT TCT TCC AAT CTT TAC AGT GCG Thr Gly Pro Leu Phe Thr Gly Thr Ala Ser Ser Asn Leu Tyr Ser Ala 775 780 785 790	3065
AAC TTC GAG TAT TTG GTC CCG GCC AAT GCC GAT CCT GTT GTT ACT ACA Asn Phe Glu Tyr Leu Val Pro Ala Asn Ala Asp Pro Val Val Thr Thr 795 800 805	3113
CAG AAT ATT ATC GTT ACA GGA CAG GGT GAA GTT GTA ATC CCC GGT GGT Gln Asn Ile Ile Val Thr Gly Gln Gly Glu Val Val Ile Pro Gly Gly 810 815 820	3161
GTT TAC GAC TAT TGC ATT ACG AAC CCG GAA CCT GCA TCC GGA AAG ATG Val Tyr Asp Tyr Cys Ile Thr Asn Pro Glu Pro Ala Ser Gly Lys Met 825 830 835	3209
TGG ATC GCA GGA GAT GGA GGC AAC CAG CCT GCA CGT TAT GAC GAT TTC Trp Ile Ala Gly Asp Gly Gly Asn Gln Pro Ala Arg Tyr Asp Asp Phe 840 845 850	3257
ACA TTC GAA GCA GGC AAG AAG TAC ACC TTC ACG ATG CGT CGC GCC GGA Thr Phe Glu Ala Gly Lys Lys Tyr Thr Phe Thr Met Arg Arg Ala Gly 855 860 865 870	3305
ATG GGA GAT GGA ACT GAT ATG GAA GTC GAA GAC GAT TCA CCT GCA AGC Met Gly Asp Gly Thr Asp Met Glu Val Glu Asp Asp Ser Pro Ala Ser 875 880 885	3353
TAT ACC TAC ACG GTG TAT CGT GAC GGC ACG AAG ATC AAG GAA GGT CTG Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Thr Lys Ile Lys Glu Gly Leu 890 895 900	3401
ACA GCT ACG ACA TTC GAA GAA GAC GGT GTA GCT GCA GGC AAT CAT GAG Thr Ala Thr Thr Phe Glu Glu Asp Gly Val Ala Ala Gly Asn His Glu 905 910 915	3449
TAT TGC GTG GAA GTT AAG TAC ACA GCC GGC GTA TCT CCG AAG GTA TGT Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Val Cys 920 925 930	3497
AAA GAC GTT ACG GTA GAA GGA TCC AAT GAA TTT GCT CCT GTA CAG AAC Lys Asp Val Thr Val Glu Gly Ser Asn Glu Phe Ala Pro Val Gln Asn 935 940 945 950	3545
CTG ACC GGT AGT TCA GTA GGT CAG AAA GTA ACG CTT AAG TGG GAT GCA Leu Thr Gly Ser Ser Val Gly Gln Lys Val Thr Leu Lys Trp Asp Ala 955 960 965	3593
CCT AAT GGT ACC CCG AAT CCG AAT CCA AAT CCG AAT CCG AAT CCG GGA Pro Asn Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn Pro Asn Pro Gly 970 975 980	3641
ACA ACA CTT TCC GAA TCA TTC GAA AAT GGT ATT CCG GCA TCT TGG AAG Thr Thr Leu Ser Glu Ser Phe Glu Asn Gly Ile Pro Ala Ser Trp Lys 985 990 995	3689
ACG ATC GAT GCA GAC GGT GAC GGG CAT GGC TGG AAA CCT GGA AAT GCT Thr Ile Asp Ala Asp Gly Asp Gly His Gly Trp Lys Pro Gly Asn Ala 1000 1005 1010	3737
CCC GGA ATC GCT GGC TAC AAT AGC AAT GGT TGT GTA TAT TCA GAG TCA Pro Gly Ile Ala Gly Tyr Asn Ser Asn Gly Cys Val Tyr Ser Glu Ser 1015 1020 1025 1030	3785

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TTC GGT CTT GGT GGT ATA GGA GTT CTT ACC CCT GAC AAC TAT CTG ATA Phe Gly Leu Gly Gly Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Ile 1035 1040 1045	3833
ACA CCG GCA TTG GAT TTG CCT AAC GGA GGT AAG TTG ACT TTC TGG GTA Thr Pro Ala Leu Asp Leu Pro Asn Gly Gly Lys Leu Thr Phe Trp Val 1050 1055 1060	3881
TGC GCA CAG GAT GCT AAT TAT GCA TCC GAG CAC TAT GCG GTG TAT GCA Cys Ala Gln Asp Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr Ala 1065 1070 1075	3929
TCT TCG ACC GGT AAC GAT GCA TCC AAC TTC ACG AAT GCT TTG TTG GAA Ser Thr Thr Gly Asn Asp Ala Ser Asn Phe Thr Asn Ala Leu Leu Glu 1080 1085 1090	3977
GAG ACG ATT ACG GCA AAA GGT GTT CGC TCG CCG AAA GCT ATT CGT GGT Glu Thr Ile Thr Ala Lys Gly Val Arg Ser Pro Lys Ala Ile Arg Gly 1095 1100 1105 1110	4025
CGT ATA CAG GGT ACT TGG CGC CAG AAG ACG GTA GAC CTT CCC GCA GGT Arg Ile Gln Gly Thr Trp Arg Gln Lys Thr Val Asp Leu Pro Ala Gly 1115 1120 1125	4073
ACG AAA TAT GTT GCT TTC CGT CAC TTC CAA AGC ACG GAT ATG TTC TAC Thr Lys Tyr Val Ala Phe Arg His Phe Gln Ser Thr Asp Met Phe Tyr 1130 1135 1140	4121
ATC GAC CTT GAT GAG GTT GAG ATC AAG GCC AAT GGC AAG CGC GCA GAC Ile Asp Leu Asp Glu Val Glu Ile Lys Ala Asn Gly Lys Arg Ala Asp 1145 1150 1155	4169
TTC ACG GAA ACG TTC GAG TCT TCT ACT CAT GGA GAG GCA CCA GCG GAA Phe Thr Glu Thr Phe Glu Ser Ser Thr His Gly Glu Ala Pro Ala Glu 1160 1165 1170	4217
TGG ACT ACT ATC GAT GCC GAT GGC GAT GGT CAG GGT TGG CTC TGT CTG Trp Thr Thr Ile Asp Ala Asp Gly Asp Gly Gln Gly Trp Leu Cys Leu 1175 1180 1185 1190	4265
TCT TCC GGA CAA TTG GAC TGG CTG ACA GCT CAT GGC GGC AGC AAC GTA Ser Ser Gly Gln Leu Asp Trp Leu Thr Ala His Gly Gly Ser Asn Val 1195 1200 1205	4313
GTA AGC TCT TTC TCA TGG AAT GGA ATG GCT TTG AAT CCT GAT AAC TAT Val Ser Ser Phe Ser Trp Asn Gly Met Ala Leu Asn Pro Asp Asn Tyr 1210 1215 1220	4361
CTC ATC TCA AAG GAT GTT ACA GGC GCA ACG AAG GTA AAG TAC TAC TAT Leu Ile Ser Lys Asp Val Thr Gly Ala Thr Lys Val Lys Tyr Tyr Tyr 1225 1230 1235	4409
GCA GTC AAC GAC GGT TTT CCC GGG GAT CAC TAT GCG GTG ATG ATC TCC Ala Val Asn Asp Gly Phe Pro Gly Asp His Tyr Ala Val Met Ile Ser 1240 1245 1250	4457
AAG ACG GGC ACG AAC GCC GGA GAC TTC ACG GTT GTT TTC GAA GAA ACG Lys Thr Gly Thr Asn Ala Gly Asp Phe Thr Val Val Phe Glu Glu Thr 1255 1260 1265 1270	4505
CCT AAC GGA ATA AAT AAG GGC GGA GCA AGA TTC GGT CTT TCC ACG GAA Pro Asn Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly Leu Ser Thr Glu 1275 1280 1285	4553

GCC AAT GGC GCC AAA CCT CAA AGT GTA TGG ATC GAG CGT ACG GTA GAT Ala Asn Gly Ala Lys Pro Gln Ser Val Trp Ile Glu Arg Thr Val Asp 1290 1295 1300	4601
TTG CCT GCA GGC ACG AAG TAT GTT GCT TTC CGT CAC TAC AAT TGC TCG Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys Ser 1305 1310 1315	4649
GAT TTG AAC TAC ATT CTT TTG GAT GAT ATT CAG TTC ACC ATG GGT GGC Asp Leu Asn Tyr Ile Leu Leu Asp Asp Ile Gln Phe Thr Met Gly Gly 1320 1325 1330	4697
AGC CCC ACC CCG ACC GAT TAT ACC TAC ACG GTG TAT CGT GAT GGT ACG Ser Pro Thr Pro Thr Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Thr 1335 1340 1345 1350	4745
AAG ATC AAG GAA GGT TTG ACC GAA ACG ACC TTC GAA GAA GAC GGC GTA Lys Ile Lys Glu Gly Leu Thr Glu Thr Phe Glu Glu Asp Gly Val 1355 1360 1365	4793
GCT ACG GGC AAT CAT GAG TAT TGC GTG GAA GTG AAG TAC ACA GCC GGC Ala Thr Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly 1370 1375 1380	4841
GTA TCT CCG AAG AAA TGT GTA GAC GTA ACT GTT AAT TCG ACA CAG TTC Val Ser Pro Lys Lys Cys Val Asp Val Thr Val Asn Ser Thr Gln Phe 1385 1390 1395	4889
AAT CCT GTA CAG AAC CTG ACG GCA GAA CAA GCT CCT AAC AGC ATG GAT Asn Pro Val Gln Asn Leu Thr Ala Glu Gln Ala Pro Asn Ser Met Asp 1400 1405 1410	4937
GCA ATC CTT AAA TGG AAT GCA CCG GCA TCT AAG CGT GCG GAA GTT CTG Ala Ile Leu Lys Trp Asn Ala Pro Ala Ser Lys Arg Ala Glu Val Leu 1415 1420 1425 1430	4985
AAC GAA GAC TTC GAA AAT GGT ATT CCT GCC TCA TGG AAG ACG ATC GAT Asn Glu Asp Phe Glu Asn Gly Ile Pro Ala Ser Trp Lys Thr Ile Asp 1435 1440 1445	5033
GCA GAC GGT GAC GGC AAC AAT TGG ACG ACG ACC CCT CCT CCC GGA GGC Ala Asp Gly Asp Gly Asn Asn Trp Thr Thr Thr Pro Pro Pro Gly Gly 1450 1455 1460	5081
TCC TCT TTT GCA GGT CAC AAC AGT GCG ATC TGT GTC TCT TCA GCT TCT Ser Ser Phe Ala Gly His Asn Ser Ala Ile Cys Val Ser Ser Ala Ser 1465 1470 1475	5129
CAT ATC AAC TTT GAA GGT CCT CAG AAC CCT GAT AAC TAT CTG GTT ACA His Ile Asn Phe Glu Gly Pro Gln Asn Pro Asp Asn Tyr Leu Val Thr 1480 1485 1490	5177
CCG GAG CTT TCT CTT CCT GGC GGA GGA ACG CTT ACT TTC TGG GTA TGT Pro Glu Leu Ser Leu Pro Gly Gly Gly Thr Leu Thr Phe Trp Val Cys 1495 1500 1505 1510	5225
GCA CAA GAT GCC AAT TAT GCA TCA GAG CAC TAT GCC GTG TAC GCA TCT Ala Gln Asp Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr Ala Ser 1515 1520 1525	5273
TCT ACG GGT AAC GAC GCT TCC AAC TTC GCC AAC GCT TTG TTG GAA GAA Ser Thr Gly Asn Asp Ala Ser Asn Phe Ala Asn Ala Leu Leu Glu Glu 1530 1535 1540	5321

GTG CTG ACG GCC AAG ACA GTT GTT ACG GCA CCT GAA GCC ATT CGT GGT Val Leu Thr Ala Lys Thr Val Val Thr Ala Pro Glu Ala Ile Arg Gly 1545 1550 1555	5369
ACT CGT GCT CAG GGC ACC TGG TAT CAA AAG ACG GTA CAG TTG CCT GCG Thr Arg Ala Gln Gly Thr Trp Tyr Gln Lys Thr Val Gln Leu Pro Ala 1560 1565 1570	5417
GGT ACT AAG TAT GTT GCC TTC CGT CAC TTC GGC TGT ACG GAC TTC TTC Gly Thr Lys Tyr Val Ala Phe Arg His Phe Gly Cys Thr Asp Phe Phe 1575 1580 1585 1590	5465
TGG ATC AAC CTT GAT GAT GTT GTA ATC ACT TCA GGG AAC GCT CCG TCT Trp Ile Asn Leu Asp Asp Val Val Ile Thr Ser Gly Asn Ala Pro Ser 1595 1600 1605	5513
TAC ACC TAT ACG ATC TAT CGT AAT AAT ACA CAG ATA GCA TCA GGC GTA Tyr Thr Tyr Thr Ile Tyr Arg Asn Asn Thr Gln Ile Ala Ser Gly Val 1610 1615 1620	5561
ACG GAG ACT ACT TAC CGA GAT CCG GAC TTG GCT ACC GGT TTT TAC ACG Thr Glu Thr Thr Tyr Arg Asp Pro Asp Leu Ala Thr Gly Phe Tyr Thr 1625 1630 1635	5609
TAC GGT GTA AAG GTT GTT TAC CCG AAC GGA GAA TCA GCT ATC GAA ACT Tyr Gly Val Lys Val Val Tyr Pro Asn Gly Glu Ser Ala Ile Glu Thr 1640 1645 1650	5657
GCT ACG TTG AAT ATC ACT TCG TTG GCA GAC GTA ACG GCT CAG AAG CCT Ala Thr Leu Asn Ile Thr Ser Leu Ala Asp Val Thr Ala Gln Lys Pro 1655 1660 1665 1670	5705
TAC ACG CTG ACA GTT GTA GGA AAG ACG ATC ACG GTA ACT TGC CAA GGC Tyr Thr Leu Thr Val Val Gly Lys Thr Ile Thr Val Thr Cys Gln Gly 1675 1680 1685	5753
GAA GCT ATG ATC TAC GAC ATG AAC GGT CGT CGT CTG GCA GCG GGT CGC Glu Ala Met Ile Tyr Asp Met Asn Gly Arg Arg Leu Ala Ala Gly Arg 1690 1695 1700	5801
AAC ACG GTT GTT TAC ACG GCT CAG GGC GGC CAC TAT GCA GTC ATG GTT Asn Thr Val Val Tyr Thr Ala Gln Gly Gly His Tyr Ala Val Met Val 1705 1710 1715	5849
GTC GTT GAC GGC AAG TCT TAC GTA GAG AAA CTC GCT GTA AAG TAAATCTGTC Val Val Asp Gly Lys Ser Tyr Val Glu Lys Leu Ala Val Lys 1720 1725 1730	5901
TTGGACTCGG AGACTTTGTG CAGACACTTT TAAGATAGGT CTGTAATTGT CTCAGAGTAT	5961
GAATCGGTGCG CCCGACTTCC TTAAAAGGAG GTCGGGCGAC TTCGTTTTTA TTATTGCTGT	6021
CCGGTAAACT TGTCAAGAGG AGACCTTTGA AAAATGAGAC CTTTGACACGG CGATTGGTGT	6081
GTATTTTGTGTT TGTTAATTCA TTGTATAATA GGGAGTTATT TTGTATATTT GAGTATTAAA	6141
AACAGCATAA TATTCCTCCC ATGGCATACC AATCCAAGAA TACCGATGAG CATGTAACAT	6201
TTGCAGACGC ACTCCTTTCA AAGCGTTATC GCAAAGCACA AAACGACTTC CTCATCAGG	6261
TTGACAGGCT TATCGATTGG CGTCCGATCA GGACGCTGAT CAACAAGAAA TACACGAAGC	6321
GACAAAATGC CATCGGCGCC CCGGCTTATG ACGTGATTCT CTTATTCAAG ATGTTGCTTC	6381

CGAAGACATG GTACAACCTC AGTGATTGTG CTTTGGAGGA GCGCATCAAT GATTCAATCA 6441
 CCTTTTCCCG ATTCTTGGGG CTATGGAAGA GGTATCTCCC GACCACAGCA CCATCAGTCG 6501
 ATTTTCGTTG GCACTGACAG AGTTGGGGCT CATGGACAAA CTATTGGCGC AGTTTAACAA 6561
 ACAACTTTTC CGCCATCACA TTTCGGTCAG GGAAAGGGTG CTTGTCGATG CAAGCCTTGT 6621
 GGAGATACGG AGCACCATCG AACGCACCTT TGGCAGTATT CGCCGGTGGT TTCATGGCGG 6681
 ACATGTGCGA TACCGGGGAC TTGCCAAGAC CCATACTCAA AACATTCTTG AAAGCATCGC 6741
 CTTTAATTTA TACAGAACCC CGGGGATAAT TATGTCCTCA TCTCTAGGAT AAGGTATAAC 6801
 CACCCTTGAG GAGCTCGTGC AAGCAGCTCC TCAAGGGGGA TTTACAATA CTTCCTCTCC 6861
 TTACCGCCAC CCTTTTCCCT CCCTCCCGGA ATTC 6895

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1732 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Arg Lys Leu Leu Leu Ile Ala Ala Ser Leu Leu Gly Val Gly
 1 5 10 15
 Leu Tyr Ala Gln Ser Ala Lys Ile Lys Leu Asp Ala Pro Thr Thr Arg
 20 25 30
 Thr Thr Cys Thr Asn Asn Ser Phe Lys Gln Phe Asp Ala Ser Phe Ser
 35 40 45
 Phe Asn Glu Val Glu Leu Thr Lys Val Glu Thr Lys Gly Gly Thr Phe
 50 55 60
 Ala Ser Val Ser Ile Pro Gly Ala Phe Pro Thr Gly Glu Val Gly Ser
 65 70 75 80
 Pro Glu Val Pro Ala Val Arg Lys Leu Ile Ala Val Pro Val Gly Ala
 85 90 95
 Thr Pro Val Val Arg Val Lys Ser Phe Thr Glu Gln Val Tyr Ser Leu
 100 105 110
 Asn Gln Tyr Gly Ser Glu Lys Leu Met Pro His Gln Pro Ser Met Ser
 115 120 125
 Lys Ser Asp Asp Pro Glu Lys Val Pro Phe Val Tyr Asn Ala Ala Ala
 130 135 140
 Tyr Ala Arg Lys Gly Phe Val Gly Gln Glu Leu Thr Gln Val Glu Met
 145 150 155 160
 Leu Gly Thr Met Arg Gly Val Arg Ile Ala Ala Leu Thr Ile Asn Pro
 165 170 175

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Val Gln Tyr Asp Val Val Ala Asn Gln Leu Lys Val Arg Asn Asn Ile
 180 185 190
 Glu Ile Glu Val Ser Phe Gln Gly Ala Asp Glu Val Ala Thr Gln Arg
 195 200 205
 Leu Tyr Asp Ala Ser Phe Ser Pro Tyr Phe Glu Thr Ala Tyr Lys Gln
 210 215 220
 Leu Phe Asn Arg Asp Val Tyr Thr Asp His Gly Asp Leu Tyr Asn Thr
 225 230 235 240
 Pro Val Arg Met Leu Val Val Ala Gly Ala Lys Phe Lys Glu Ala Leu
 245 250 255
 Lys Pro Trp Leu Thr Trp Lys Ala Gln Lys Gly Phe Tyr Leu Asp Val
 260 265 270
 His Tyr Thr Asp Glu Ala Glu Val Gly Thr Thr Asn Ala Ser Ile Lys
 275 280 285
 Ala Phe Ile His Lys Lys Tyr Asn Asp Gly Leu Ala Ala Ser Ala Ala
 290 295 300
 Pro Val Phe Leu Ala Leu Val Gly Asp Thr Asp Val Ile Ser Gly Glu
 305 310 315 320
 Lys Gly Lys Lys Thr Lys Lys Val Thr Asp Leu Tyr Tyr Ser Ala Val
 325 330 335
 Asp Gly Asp Tyr Phe Pro Glu Met Tyr Thr Phe Arg Met Ser Ala Ser
 340 345 350
 Ser Pro Glu Glu Leu Thr Asn Ile Ile Asp Lys Val Leu Met Tyr Glu
 355 360 365
 Lys Ala Thr Met Pro Asp Lys Ser Tyr Leu Glu Lys Val Leu Leu Ile
 370 375 380
 Ala Gly Ala Asp Tyr Ser Trp Asn Ser Gln Val Gly Gln Pro Thr Ile
 385 390 395 400
 Lys Tyr Gly Met Gln Tyr Tyr Tyr Asn Gln Glu His Gly Tyr Thr Asp
 405 410 415
 Val Tyr Asn Tyr Leu Lys Ala Pro Tyr Thr Gly Cys Tyr Ser His Leu
 420 425 430
 Asn Thr Gly Val Ser Phe Ala Asn Tyr Thr Ala His Gly Ser Glu Thr
 435 440 445
 Ala Trp Ala Asp Pro Leu Leu Thr Thr Ser Gln Leu Lys Ala Leu Thr
 450 455 460
 Asn Lys Asp Lys Tyr Phe Leu Ala Ile Gly Asn Cys Cys Ile Thr Ala
 465 470 475 480
 Gln Phe Asp Tyr Val Gln Pro Cys Phe Gly Glu Val Ile Thr Arg Val
 485 490 495
 Lys Glu Lys Gly Ala Tyr Ala Tyr Ile Gly Ser Ser Pro Asn Ser Tyr
 500 505 510

78

Trp Gly Glu Asp Tyr Tyr Trp Ser Val Gly Ala Asn Ala Val Phe Gly
 515 520 525
 Val Gln Pro Thr Phe Glu Gly Thr Ser Met Gly Ser Tyr Asp Ala Thr
 530 535 540
 Phe Leu Glu Asp Ser Tyr Asn Thr Val Asn Ser Ile Met Trp Ala Gly
 545 550 555 560
 Asn Leu Ala Ala Thr His Ala Gly Asn Ile Gly Asn Ile Thr His Ile
 565 570 575
 Gly Ala His Tyr Tyr Trp Glu Ala Tyr His Val Leu Gly Asp Gly Ser
 580 585 590
 Val Met Pro Tyr Arg Ala Met Pro Lys Thr Asn Thr Tyr Thr Leu Pro
 595 600 605
 Ala Ser Leu Pro Gln Asn Gln Ala Ser Tyr Ser Ile Gln Ala Ser Ala
 610 615 620
 Gly Ser Tyr Val Ala Ile Ser Lys Asp Gly Val Leu Tyr Gly Thr Gly
 625 630 635 640
 Val Ala Asn Ala Ser Gly Val Ala Thr Val Ser Met Thr Lys Gln Ile
 645 650 655
 Thr Glu Asn Gly Asn Tyr Asp Val Val Ile Thr Arg Ser Asn Tyr Leu
 660 665 670
 Pro Val Ile Lys Gln Ile Gln Val Gly Glu Pro Ser Pro Tyr Gln Pro
 675 680 685
 Val Ser Asn Leu Thr Ala Thr Thr Gln Gly Gln Lys Val Thr Leu Lys
 690 695 700
 Trp Glu Ala Pro Ser Ala Lys Lys Ala Glu Gly Ser Arg Glu Val Lys
 705 710 715 720
 Arg Ile Gly Asp Gly Leu Phe Val Thr Ile Glu Pro Ala Asn Asp Val
 725 730 735
 Arg Ala Asn Glu Ala Lys Val Val Leu Ala Ala Asp Asn Val Trp Gly
 740 745 750
 Asp Asn Thr Gly Tyr Gln Phe Leu Leu Asp Ala Asp His Asn Thr Phe
 755 760 765
 Gly Ser Val Ile Pro Ala Thr Gly Pro Leu Phe Thr Gly Thr Ala Ser
 770 775 780
 Ser Asn Leu Tyr Ser Ala Asn Phe Glu Tyr Leu Val Pro Ala Asn Ala
 785 790 795 800
 Asp Pro Val Val Thr Thr Gln Asn Ile Ile Val Thr Gly Gln Gly Glu
 805 810 815
 Val Val Ile Pro Gly Gly Val Tyr Asp Tyr Cys Ile Thr Asn Pro Glu
 820 825 830
 Pro Ala Ser Gly Lys Met Trp Ile Ala Gly Asp Gly Gly Asn Gln Pro
 835 840 845

Ala Arg Tyr Asp Asp Phe Thr Phe Glu Ala Gly Lys Lys Tyr Thr Phe
 850 855 860
 Thr Met Arg Arg Ala Gly Met Gly Asp Gly Thr Asp Met Glu Val Glu
 865 870 875 880
 Asp Asp Ser Pro Ala Ser Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Thr
 885 890 895
 Lys Ile Lys Glu Gly Leu Thr Ala Thr Thr Phe Glu Glu Asp Gly Val
 900 905 910
 Ala Ala Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly
 915 920 925
 Val Ser Pro Lys Val Cys Lys Asp Val Thr Val Glu Gly Ser Asn Glu
 930 935 940
 Phe Ala Pro Val Gln Asn Leu Thr Gly Ser Ser Val Gly Gln Lys Val
 945 950 955 960
 Thr Leu Lys Trp Asp Ala Pro Asn Gly Thr Pro Asn Pro Asn Pro Asn
 965 970 975
 Pro Asn Pro Asn Pro Gly Thr Thr Leu Ser Glu Ser Phe Glu Asn Gly
 980 985 990
 Ile Pro Ala Ser Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly His Gly
 995 1000 1005
 Trp Lys Pro Gly Asn Ala Pro Gly Ile Ala Gly Tyr Asn Ser Asn Gly
 1010 1015 1020
 Cys Val Tyr Ser Glu Ser Phe Gly Leu Gly Gly Ile Gly Val Leu Thr
 1025 1030 1035 1040
 Pro Asp Asn Tyr Leu Ile Thr Pro Ala Leu Asp Leu Pro Asn Gly Gly
 1045 1050 1055
 Lys Leu Thr Phe Trp Val Cys Ala Gln Asp Ala Asn Tyr Ala Ser Glu
 1060 1065 1070
 His Tyr Ala Val Tyr Ala Ser Ser Thr Gly Asn Asp Ala Ser Asn Phe
 1075 1080 1085
 Thr Asn Ala Leu Leu Glu Glu Thr Ile Thr Ala Lys Gly Val Arg Ser
 1090 1095 1100
 Pro Lys Ala Ile Arg Gly Arg Ile Gln Gly Thr Trp Arg Gln Lys Thr
 1105 1110 1115 1120
 Val Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Phe Gln
 1125 1130 1135
 Ser Thr Asp Met Phe Tyr Ile Asp Leu Asp Glu Val Glu Ile Lys Ala
 1140 1145 1150
 Asn Gly Lys Arg Ala Asp Phe Thr Glu Thr Phe Glu Ser Ser Thr His
 1155 1160 1165
 Gly Glu Ala Pro Ala Glu Trp Thr Thr Ile Asp Ala Asp Gly Asp Gly
 1170 1175 1180

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Gln Gly Trp Leu Cys Leu Ser Ser Gly Gln Leu Asp Trp Leu Thr Ala
 1185 1190 1195 1200
 His Gly Gly Ser Asn Val Val Ser Ser Phe Ser Trp Asn Gly Met Ala
 1205 1210 1215
 Leu Asn Pro Asp Asn Tyr Leu Ile Ser Lys Asp Val Thr Gly Ala Thr
 1220 1225 1230
 Lys Val Lys Tyr Tyr Tyr Ala Val Asn Asp Gly Phe Pro Gly Asp His
 1235 1240 1245
 Tyr Ala Val Met Ile Ser Lys Thr Gly Thr Asn Ala Gly Asp Phe Thr
 1250 1255 1260
 Val Val Phe Glu Glu Thr Pro Asn Gly Ile Asn Lys Gly Gly Ala Arg
 1265 1270 1275 1280
 Phe Gly Leu Ser Thr Glu Ala Asn Gly Ala Lys Pro Gln Ser Val Trp
 1285 1290 1295
 Ile Glu Arg Thr Val Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe
 1300 1305 1310
 Arg His Tyr Asn Cys Ser Asp Leu Asn Tyr Ile Leu Leu Asp Asp Ile
 1315 1320 1325
 Gln Phe Thr Met Gly Gly Ser Pro Thr Pro Thr Asp Tyr Thr Tyr Thr
 1330 1335 1340
 Val Tyr Arg Asp Gly Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr Thr
 1345 1350 1355 1360
 Phe Glu Glu Asp Gly Val Ala Thr Gly Asn His Glu Tyr Cys Val Glu
 1365 1370 1375
 Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Lys Cys Val Asp Val Thr
 1380 1385 1390
 Val Asn Ser Thr Gln Phe Asn Pro Val Gln Asn Leu Thr Ala Glu Gln
 1395 1400 1405
 Ala Pro Asn Ser Met Asp Ala Ile Leu Lys Trp Asn Ala Pro Ala Ser
 1410 1415 1420
 Lys Arg Ala Glu Val Leu Asn Glu Asp Phe Glu Asn Gly Ile Pro Ala
 1425 1430 1435 1440
 Ser Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Asn Asn Trp Thr Thr
 1445 1450 1455
 Thr Pro Pro Pro Gly Gly Ser Ser Phe Ala Gly His Asn Ser Ala Ile
 1460 1465 1470
 Cys Val Ser Ser Ala Ser His Ile Asn Phe Glu Gly Pro Gln Asn Pro
 1475 1480 1485
 Asp Asn Tyr Leu Val Thr Pro Glu Leu Ser Leu Pro Gly Gly Gly Thr
 1490 1495 1500
 Leu Thr Phe Trp Val Cys Ala Gln Asp Ala Asn Tyr Ala Ser Glu His
 1505 1510 1515 1520

81

Tyr Ala Val Tyr Ala Ser Ser Thr Gly Asn Asp Ala Ser Asn Phe Ala
 1525 1530 1535
 Asn Ala Leu Leu Glu Glu Val Leu Thr Ala Lys Thr Val Val Thr Ala
 1540 1545 1550
 Pro Glu Ala Ile Arg Gly Thr Arg Ala Gln Gly Thr Trp Tyr Gln Lys
 1555 1560 1565
 Thr Val Gln Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Phe
 1570 1575 1580
 Gly Cys Thr Asp Phe Phe Trp Ile Asn Leu Asp Asp Val Val Ile Thr
 1585 1590 1595 1600
 Ser Gly Asn Ala Pro Ser Tyr Thr Tyr Thr Ile Tyr Arg Asn Asn Thr
 1605 1610 1615
 Gln Ile Ala Ser Gly Val Thr Glu Thr Thr Tyr Arg Asp Pro Asp Leu
 1620 1625 1630
 Ala Thr Gly Phe Tyr Thr Tyr Gly Val Lys Val Val Tyr Pro Asn Gly
 1635 1640 1645
 Glu Ser Ala Ile Glu Thr Ala Thr Leu Asn Ile Thr Ser Leu Ala Asp
 1650 1655 1660
 Val Thr Ala Gln Lys Pro Tyr Thr Leu Thr Val Val Gly Lys Thr Ile
 1665 1670 1675 1680
 Thr Val Thr Cys Gln Gly Glu Ala Met Ile Tyr Asp Met Asn Gly Arg
 1685 1690 1695
 Arg Leu Ala Ala Gly Arg Asn Thr Val Val Tyr Thr Ala Gln Gly Gly
 1700 1705 1710
 His Tyr Ala Val Met Val Val Val Asp Gly Lys Ser Tyr Val Glu Lys
 1715 1720 1725
 Leu Ala Val Lys
 1730

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAATGGGAG ATGGAACT

18

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs

82

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTAACCCGTA TTGTCTCC

18

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8588 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 365..8248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATATCCGGC TCTTCGGCAG AGAATGCGAG AGATTCAGGA TATATCGCAA CGGCCTTGTC	60
AAGATCGAGG CCTCTTTAGG TCATGGATAT AACGTGAGTT CGATGTAAGC TTTTCGGCCT	120
TTCCATCATA CAATCGATTC GATTCTCTTT GGA CTCAATA AAAAATATAA AATACTCAAA	180
GAGTTGGCAT ATA ACTTTGC CTCAGTGGCG AGTGGGTTTT TCGGCCAATT CCTAAAGAAG	240
AAAATAGCTG TTTGTATCTT TTTGCGAAAA AAGTTTGGCG GATTAAGATT AAAAACATAT	300
CTTTCGGGCG ATAGTGGTAG AGCACTATCT TGCGAAACAT TAATCTTTAA TACTTTCAAA	360
AGGT ATG AGA AAA TTG AAT TCT TTA TTT TCG CTC GCC GTC CTA TTA TCC	409
Met Arg Lys Leu Asn Ser Leu Phe Ser Leu Ala Val Leu Leu Ser	
1 5 10 15	
CTA TTG TGT TGG GGA CAG ACG GCT GCC GCA CAG GGA GGG CCG AAG ACT	457
Leu Leu Cys Trp Gly Gln Thr Ala Ala Ala Gln Gly Gly Pro Lys Thr	
20 25 30	
GCT CCT TCT GTG ACG CAC CAA GCG GTG CAG AAA GGT ATT CGA ACA TCC	505
Ala Pro Ser Val Thr His Gln Ala Val Gln Lys Gly Ile Arg Thr Ser	
35 40 45	
AAG GTT AAG GAT CTC CGA GAT CCG ATT CCT GCC GGT ATG GCA CGA ATT	553
Lys Val Lys Asp Leu Arg Asp Pro Ile Pro Ala Gly Met Ala Arg Ile	
50 55 60	
ATC TTG GAG GCT CAC GAT GTA TGG GAA GAC GGC ACA GGC TAT CAA ATG	601
Ile Leu Glu Ala His Asp Val Trp Glu Asp Gly Thr Gly Tyr Gln Met	
65 70 75	

83

CTT TGG GAT GCA GAT CAC AAT CAG TAC GGC GCA TCC ATT CCC GAA GAA Leu Trp Asp Ala Asp His Asn Gln Tyr Gly Ala Ser Ile Pro Glu Glu 80 85 90 95	649
TCT TTT TGG TTT GCC AAC GGA ACG ATC CCG GCC GGT CTT TAC GAT CCT Ser Phe Trp Phe Ala Asn Gly Thr Ile Pro Ala Gly Leu Tyr Asp Pro 100 105 110	697
TTC GAG TAT AAA GTT CCG GTC AAT GCC GAT GCA TCT TTT TCT CCC ACG Phe Glu Tyr Lys Val Pro Val Asn Ala Asp Ala Ser Phe Ser Pro Thr 115 120 125	745
AAT TTC GTG CTT GAT GGA ACA GCA TCA GCC GAT ATT CCT GCC GGC ACT Asn Phe Val Leu Asp Gly Thr Ala Ser Ala Asp Ile Pro Ala Gly Thr 130 135 140	793
TAT GAC TAT GTA ATC ATT AAC CCC AAT CCT GGC ATA ATA TAT ATA GTA Tyr Asp Tyr Val Ile Ile Asn Pro Asn Pro Gly Ile Ile Tyr Ile Val 145 150 155	841
GGA GAG GGT GTC TCC AAA GGT AAC GAT TAT GTG GTA GAG GCC GGT AAG Gly Glu Gly Val Ser Lys Gly Asn Asp Tyr Val Val Glu Ala Gly Lys 160 165 170 175	889
ACT TAT CAT TTC ACT GTC CAA CGA CAA GGC CCC GGC GAT GCT GCG TCC Thr Tyr His Phe Thr Val Gln Arg Gln Gly Pro Gly Asp Ala Ala Ser 180 185 190	937
GTT GTA GTG ACC GGA GAA GGT GGC AAT GAA TTC GCT CCC GTA CAG AAT Val Val Val Thr Gly Glu Gly Gly Asn Glu Phe Ala Pro Val Gln Asn 195 200 205	985
CTC CAA TGG TCT GTA TCT GGG CAG ACA GTG ACC CTC ACT TGG CAA GCC Leu Gln Trp Ser Val Ser Gly Gln Thr Val Thr Leu Thr Trp Gln Ala 210 215 220	1033
CCC GCA TCC GAC AAA CGG ACT TAT GTG TTG AAC GAA AGC TTC GAT ACG Pro Ala Ser Asp Lys Arg Thr Tyr Val Leu Asn Glu Ser Phe Asp Thr 225 230 235	1081
CAA ACG CTT CCT AAC GGC TGG ACA ATG ATC GAT GCT GAT GGT GAT GGT Gln Thr Leu Pro Asn Gly Trp Thr Met Ile Asp Ala Asp Gly Asp Gly 240 245 250 255	1129
CAC AAT TGG CTA TCT ACA ATA AAC GTT TAC AAC ACT GCT ACT CAT ACA His Asn Trp Leu Ser Thr Ile Asn Val Tyr Asn Thr Ala Thr His Thr 260 265 270	1177
GGT GAC GGT GCT ATG TTT AGC AAA TCA TGG ACT GCT AGC GGT GGT GCA Gly Asp Gly Ala Met Phe Ser Lys Ser Trp Thr Ala Ser Gly Gly Ala 275 280 285	1225
AAA ATT GAT TTG AGT CCT GAC AAC TAT TTG GTA ACT CCA AAG GTT ACG Lys Ile Asp Leu Ser Pro Asp Asn Tyr Leu Val Thr Pro Lys Val Thr 290 295 300	1273
GTT CCT GAG AAT GGT AAA CTT TCT TAT TGG GTT TCA TCT CAA GTG CCT Val Pro Glu Asn Gly Lys Leu Ser Tyr Trp Val Ser Ser Gln Val Pro 305 310 315	1321
TGG ACT AAT GAG CAT TAT GGA GTG TTC TTG TCC ACA ACC GGA AAC GAG Trp Thr Asn Glu His Tyr Gly Val Phe Leu Ser Thr Thr Gly Asn Glu 320 325 330 335	1369

GCT GCA AAC TTT ACG ATA AAG CTA CTG GAA GAA ACC CTC GGA TCC GAC Ala Ala Asn Phe Thr Ile Lys Leu Leu Glu Glu Thr Leu Gly Ser Asp 340 345 350	1417
AAA CCT GCT CCG ATG AAC TTG GTG AAG AGT GAA GGA GTA AAG CTT CCT Lys Pro Ala Pro Met Asn Leu Val Lys Ser Glu Gly Val Lys Leu Pro 355 360 365	1465
GCA CCT TAT CAG GAA AGA ACC ATC GAT CTC TCT GCC TAT GCC GGA CAA Ala Pro Tyr Gln Glu Arg Thr Ile Asp Leu Ser Ala Tyr Ala Gly Gln 370 375 380	1513
CAG GTG TAC TTG GCA TTC CGT CAT TTC AAC TCT ACA GGT ATA TTC CGT Gln Val Tyr Leu Ala Phe Arg His Phe Asn Ser Thr Gly Ile Phe Arg 385 390 395	1561
CTT TAT CTT GAT GAT GTG GCT GTT TCT GGT GAA GGT TCT TCC AAC GAC Leu Tyr Leu Asp Asp Val Ala Val Ser Gly Glu Gly Ser Ser Asn Asp 400 405 410 415	1609
TAC ACG TAC ACG GTA TAT CGT GAC AAT GTT GTT ATT GCC CAG AAT CTC Tyr Thr Tyr Thr Val Tyr Arg Asp Asn Val Val Ile Ala Gln Asn Leu 420 425 430	1657
GCG GCA ACG ACA TTC AAT CAG GAA AAT GTA GCT CCC GGC CAG TAT AAC Ala Ala Thr Thr Phe Asn Gln Glu Asn Val Ala Pro Gly Gln Tyr Asn 435 440 445	1705
TAC TGT GTT GAA GTT AAG TAC ACA GCC GGC GTA TCT CCG AAG GTA TGT Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Val Cys 450 455 460	1753
AAA GAC GTT ACG GTA GAA GGA TCC AAC GAA TTT GCT CAT GTA CAG AAC Lys Asp Val Thr Val Glu Gly Ser Asn Glu Phe Ala His Val Gln Asn 465 470 475	1801
CTG ACC GGT AGT GCA GTA GGT CAG AAA GTA ACG CTT AAG TGG GAT GCA Leu Thr Gly Ser Ala Val Gly Gln Lys Val Thr Leu Lys Trp Asp Ala 480 485 490 495	1849
CCT AAT GGT ACC CCG AAT CCG AAT CCC GGA ACA ACA ACA CTT TCC GAA Pro Asn Gly Thr Pro Asn Pro Asn Pro Gly Thr Thr Thr Leu Ser Glu 500 505 510	1897
TCA TTC GAA AAT GGT ATT CCT GCC TCA TGG AAG ACG ATC GAT GCA GAC Ser Phe Glu Asn Gly Ile Pro Ala Ser Trp Lys Thr Ile Asp Ala Asp 515 520 525	1945
GGT GAC GGC AAC AAT TGG ACG ACG ACC CCT CCT CCC GGA GGC ACC TCT Gly Asp Gly Asn Asn Trp Thr Thr Thr Pro Pro Pro Gly Gly Thr Ser 530 535 540	1993
TTT GCA GGT CAC AAC AGT GCA ATC TGT GCC TCT TCG GCT TCT TAT ATC Phe Ala Gly His Asn Ser Ala Ile Cys Ala Ser Ser Ala Ser Tyr Ile 545 550 555	2041
AAC TTT GAA GGT CCT CAG AAC CCT GAT AAC TAT CTG GTT ACA CCG GAG Asn Phe Glu Gly Pro Gln Asn Pro Asp Asn Tyr Leu Val Thr Pro Glu 560 565 570 575	2089
CTA TCT CTT CCT AAC GGA GGA ACG CTT ACT TTC TGG GTA TGT GCA CAA Leu Ser Leu Pro Asn Gly Gly Thr Leu Thr Phe Trp Val Cys Ala Gln 580 585 590	2137

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GAT GCC AAT TAT GCA TCA GAG CAC TAT GCC GTG TAC GCA TCT TCT ACG Asp Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr Ala Ser Ser Thr 595 600 605	2185
GGT AAC GAC GCT TCC AAC TTC GCC AAC GCT TTG TTG GAA GAA GTG CTG Gly Asn Asp Ala Ser Asn Phe Ala Asn Ala Leu Leu Glu Glu Val Leu 610 615 620	2233
ACG GCC AAG ACA GTT GTT ACG GCA CCT GAA GCC ATT CGT GGC ACT CGT Thr Ala Lys Thr Val Val Thr Ala Pro Glu Ala Ile Arg Gly Thr Arg 625 630 635	2281
GTT CAG GGC ACC TGG TAT CAA AAG ACG GTA CAG TTG CCT GCG GGT ACT Val Gln Gly Thr Trp Tyr Gln Lys Thr Val Gln Leu Pro Ala Gly Thr 640 645 650 655	2329
AAG TAT GTT GCT TTC CGT CAC TTC GGC TGT ACG GAC TTC TTC TGG ATT Lys Tyr Val Ala Phe Arg His Phe Gly Cys Thr Asp Phe Phe Trp Ile 660 665 670	2377
AAC CTT GAT GAT GTT GAG ATC AAG GCC AAC GGC AAG CGC GCA GAC TTC Asn Leu Asp Asp Val Glu Ile Lys Ala Asn Gly Lys Arg Ala Asp Phe 675 680 685	2425
ACG GAA ACG TTC GAG TCT TCT ACT CAT GGA GAG GCA CCG GCG GAA TGG Thr Glu Thr Phe Glu Ser Ser Thr His Gly Glu Ala Pro Ala Glu Trp 690 695 700	2473
ACT ACT ATC GAT GCC GAT GGC GAT GGT CAG GGT TGG CTC TGT CTG TCT Thr Thr Ile Asp Ala Asp Gly Asp Gly Gln Gly Trp Leu Cys Leu Ser 705 710 715	2521
TCC GGA CAA TTG GAC TGG CTG ACA GCT CAT GGC GGC ACC AAC GTA GTA Ser Gly Gln Leu Asp Trp Leu Thr Ala His Gly Gly Thr Asn Val Val 720 725 730 735	2569
GCC TCT TTC TCA TGG AAT GGA ATG GCT TTG AAT CCT GAT AAC TAT CTC Ala Ser Phe Ser Trp Asn Gly Met Ala Leu Asn Pro Asp Asn Tyr Leu 740 745 750	2617
ATC TCA AAG GAT GTT ACA GGC GCA ACT AAG GTA AAG TAC TAC TAT GCA Ile Ser Lys Asp Val Thr Gly Ala Thr Lys Val Lys Tyr Tyr Tyr Ala 755 760 765	2665
GTC AAC GAC GGT TTT CCC GGG GAT CAC TAT GCG GTG ATG ATC TCC AAG Val Asn Asp Gly Phe Pro Gly Asp His Tyr Ala Val Met Ile Ser Lys 770 775 780	2713
ACG GGC ACG AAC GCC GGA GAC TTC ACG GTT GTT TTC GAA GAA ACG CCT Thr Gly Thr Asn Ala Gly Asp Phe Thr Val Val Phe Glu Glu Thr Pro 785 790 795	2761
AAC GGA ATA AAT AAG GGC GGA GCA AGA TTC GGT CTT TCC ACG GAA GCC Asn Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly Leu Ser Thr Glu Ala 800 805 810 815	2809
GAT GGC GCC AAA CCT CAA AGT GTA TGG ATC GAG CGT ACG GTA GAT TTG Asp Gly Ala Lys Pro Gln Ser Val Trp Ile Glu Arg Thr Val Asp Leu 820 825 830	2857
CCT GCG GGT ACT AAG TAT GTT GCT TTC CGT CAC TAC AAT TGC TCG GAT Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys Ser Asp 835 840 845	2905

TTG AAC TAC ATT CTT TTG GAT GAT ATT CAG TTC ACC ATG GGT GGC AGC Leu Asn Tyr Ile Leu Leu Asp Asp Ile Gln Phe Thr Met Gly Gly Ser 850 855 860	2953
CCC ACC CCG ACC GAT TAT ACC TAC ACG GTG TAT CGT GAC GGT ACG AAG Pro Thr Pro Thr Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Thr Lys 865 870 875	3001
ATC AAG GAA GGT CTG ACC GAA ACG ACC TTC GAA GAA GAC GGT GTA GCT Ile Lys Glu Gly Leu Thr Glu Thr Thr Phe Glu Glu Asp Gly Val Ala 880 885 890 895	3049
ACG GGC AAC CAT GAG TAT TGC GTG GAA GTG AAG TAC ACA GCC GGC GTA Thr Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly Val 900 905 910	3097
TCT CCG AAA GAG TGT GTA AAC GTA ACT GTT GAT CCT GTG CAG TTC AAT Ser Pro Lys Glu Cys Val Asn Val Thr Val Asp Pro Val Gln Phe Asn 915 920 925	3145
CCT GTA CAG AAC CTG ACC GGT AGT GCA GTC GGC CAG AAA GTA ACG CTT Pro Val Gln Asn Leu Thr Gly Ser Ala Val Gly Gln Lys Val Thr Leu 930 935 940	3193
AAG TGG GAT GCA CCT AAT GGT ACC CCG AAT CCA AAT CCA AAT CCG AAT Lys Trp Asp Ala Pro Asn Gly Thr Pro Asn Pro Asn Pro Asn 945 950 955	3241
CCG GGA ACA ACA ACA CTT TCC GAA TCA TTC GAA AAT GGT ATT CCT GCC Pro Gly Thr Thr Thr Leu Ser Glu Ser Phe Glu Asn Gly Ile Pro Ala 960 965 970 975	3289
TCA TGG AAG ACG ATC GAT GCA GAC GGT GAC GGC AAC AAT TGG ACG ACG Ser Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Asn Asn Trp Thr 980 985 990	3337
ACC CCT CCT CCC GGA GGC ACC TCT TTT GCA GGT CAC AAC AGT GCG ATC Thr Pro Pro Gly Gly Thr Ser Phe Ala Gly His Asn Ser Ala Ile 995 1000 1005	3385
TGT GCC TCT TCG GCT TCT TAT ATC AAC TTT GAA GGC CCT CAG AAC CCT Cys Ala Ser Ser Ala Ser Tyr Ile Asn Phe Glu Gly Pro Gln Asn Pro 1010 1015 1020	3433
GAT AAC TAT CTG GTT ACA CCG GAG CTA TCT CTT CCT AAC GGA GGA ACG Asp Asn Tyr Leu Val Thr Pro Glu Leu Ser Leu Pro Asn Gly Gly Thr 1025 1030 1035	3481
CTT ACT TTC TGG GTA TGT GCA CAA GAT GCC AAT TAT GCA TCA GAG CAC Leu Thr Phe Trp Val Cys Ala Gln Asp Ala Asn Tyr Ala Ser Glu His 1040 1045 1050 1055	3529
TAT GCC GTG TAT GCA TCT TCT ACG GGT AAC GAC GCT TCC AAC TTC GCC Tyr Ala Val Tyr Ala Ser Ser Thr Gly Asn Asp Ala Ser Asn Phe Ala 1060 1065 1070	3577
AAC GCT TTG TTG GAA GAA GTG CTG ACG GCC AAG ACA GTT GTT ACG GCA Asn Ala Leu Leu Glu Glu Val Leu Thr Ala Lys Thr Val Val Thr Ala 1075 1080 1085	3625
CCT GAA GCC ATT CGT GGC ACT CGT GTT CAG GGC ACC TGG TAT CAA AAG Pro Glu Ala Ile Arg Gly Thr Arg Val Gln Gly Thr Trp Tyr Gln Lys 1090 1095 1100	3673

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ACG GTA CAG TTG CCT GCG GGT ACT AAG TAT GTT GCT TTC CGT CAC TTC Thr Val Gln Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Phe 1105 1110 1115	3721
GGC TGT ACG GAC TTC TTC TGG ATC AAC CTT GAT GAT GTT GAG ATC AAG Gly Cys Thr Asp Phe Phe Trp Ile Asn Leu Asp Asp Val Glu Ile Lys 1120 1125 1130 1135	3769
GCC AAC GGC AAG CGC GCA GAC TTC ACG GAA ACG TTC GAG TCT TCT ACT Ala Asn Gly Lys Arg Ala Asp Phe Thr Glu Thr Phe Glu Ser Ser Thr 1140 1145 1150	3817
CAT GGA GAG GCA CCG GCG GAA TGG ACT ACT ATC GAT GCC GAT GGC GAT His Gly Glu Ala Pro Ala Glu Trp Thr Thr Ile Asp Ala Asp Gly Asp 1155 1160 1165	3865
GGT CAG GGT TGG CTC TGT CTG TCT TCC GGA CAA TTG GGC TGG CTG ACA Gly Gln Gly Trp Leu Cys Leu Ser Ser Gly Gln Leu Gly Trp Leu Thr 1170 1175 1180	3913
GCT CAT GGC GGC ACC AAC GTA GTA GCC TCT TTC TCA TGG AAT GGA ATG Ala His Gly Gly Thr Asn Val Val Ala Ser Phe Ser Trp Asn Gly Met 1185 1190 1195	3961
GCT TTG AAT CCT GAT AAC TAT CTC ATC TCA AAG GAT GTT ACA GGC GCA Ala Leu Asn Pro Asp Asn Tyr Leu Ile Ser Lys Asp Val Thr Gly Ala 1200 1205 1210 1215	4009
ACT AAG GTA AAG TAC TAC TAT GCA GTC AAC GAC GGT TTT CCC GGG GAT Thr Lys Val Lys Tyr Tyr Tyr Ala Val Asn Asp Gly Phe Pro Gly Asp 1220 1225 1230	4057
CAC TAT GCG GTG ATG ATC TCC AAG ACG GGC ACG AAC GCC GGA GAC TTC His Tyr Ala Val Met Ile Ser Lys Thr Gly Thr Asn Ala Gly Asp Phe 1235 1240 1245	4105
ACG GTT GTT TTC GAA GAA ACG CCT AAC GGA ATA AAT AAG GGC GGA GCA Thr Val Val Phe Glu Glu Thr Pro Asn Gly Ile Asn Lys Gly Gly Ala 1250 1255 1260	4153
AGA TTC GGT CTT TCC ACG GAA GCC GAT GGC GCC AAA CCT CAA AGT GTA Arg Phe Gly Leu Ser Thr Glu Ala Asp Gly Ala Lys Pro Gln Ser Val 1265 1270 1275	4201
TGG ATC GAG CGT ACG GTA GAT TTG CCT GCG GGT ACT AAG TAT GTT GCT Trp Ile Glu Arg Thr Val Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala 1280 1285 1290 1295	4249
TTC CGT CAC TAC AAT TGC TCG GAT TTG AAC TAC ATT CTT TTG GAT GAT Phe Arg His Tyr Asn Cys Ser Asp Leu Asn Tyr Ile Leu Leu Asp Asp 1300 1305 1310	4297
ATT CAG TTC ACC ATG GGT GGC AGC CCC ACC CCG ACC GAT TAT ACC TAC Ile Gln Phe Thr Met Gly Gly Ser Pro Thr Pro Thr Asp Tyr Thr Tyr 1315 1320 1325	4345
ACG GTG TAT CGT GAC GGT ACG AAG ATC AAG GAA GGT CTG ACC GAA ACG Thr Val Tyr Arg Asp Gly Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr 1330 1335 1340	4393
ACC TTC GAA GAA GAC GGT GTA GCT ACG GGC AAC CAT GAG TAT TGC GTG Thr Phe Glu Glu Asp Gly Val Ala Thr Gly Asn His Glu Tyr Cys Val 1345 1350 1355	4441

GAA GTG AAG TAC ACA GCC GGC GTA TCT CCG AAA GAG TGT GTA AAC GTA Glu Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Glu Cys Val Asn Val 1360 1365 1370 1375	4489
ACT GTT GAT CCT GTG CAG TTC AAT CCT GTA CAG AAC CTG ACC GGT AGT Thr Val Asp Pro Val Gln Phe Asn Pro Val Gln Asn Leu Thr Gly Ser 1380 1385 1390	4537
GCA GTC GGC CAG AAA GTA ACG CTT AAG TGG GAT GCA CCT AAT GGT ACC Ala Val Gly Gln Lys Val Thr Leu Lys Trp Asp Ala Pro Asn Gly Thr 1395 1400 1405	4585
CCG AAT CCA AAT CCA AAT CCG AAT CCG GGA ACA ACA ACA CTT TCC GAA Pro Asn Pro Asn Pro Asn Pro Asn Pro Gly Thr Thr Thr Leu Ser Glu 1410 1415 1420	4633
TCA TTC GAA AAT GGT ATT CCT GCC TCA TGG AAG ACG ATC GAT GCA GAC Ser Phe Glu Asn Gly Ile Pro Ala Ser Trp Lys Thr Ile Asp Ala Asp 1425 1430 1435	4681
GGT GAC GGC AAC AAT TGG ACG ACG ACC CCT CCT CCC GGA GGC ACC TCT Gly Asp Gly Asn Asn Trp Thr Thr Pro Pro Gly Gly Thr Ser 1440 1445 1450 1455	4729
TTT GCA GGT CAC AAC AGT GCG ATC TGT GCC TCT TCG GCT TCT TAT ATC Phe Ala Gly His Asn Ser Ala Ile Cys Ala Ser Ser Ala Ser Tyr Ile 1460 1465 1470	4777
AAC TTT GAA GGC CCT CAG AAC CCT GAT AAC TAT CTG GTT ACA CCG GAG Asn Phe Glu Gly Pro Gln Asn Pro Asp Asn Tyr Leu Val Thr Pro Glu 1475 1480 1485	4825
CTA TCT CTT CCT AAC GGA GGA ACG CTT ACT TTC TGG GTA TGT GCA CAA Leu Ser Leu Pro Asn Gly Gly Thr Leu Thr Phe Trp Val Cys Ala Gln 1490 1495 1500	4873
GAT GCC AAT TAT GCA TCA GAG CAC TAT GCC GTG TAT GCA TCT TCT ACG Asp Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr Ala Ser Ser Thr 1505 1510 1515	4921
GGT AAC GAC GCT TCC AAC TTC GCC AAC GCT TTG TTG GAA GAA GTG CTG Gly Asn Asp Ala Ser Asn Phe Ala Asn Ala Leu Leu Glu Glu Val Leu 1520 1525 1530 1535	4969
ACG GCC AAG ACA GTT GTT ACG GCA CCT GAA GCC ATT CGT GGC ACT CGT Thr Ala Lys Thr Val Val Thr Ala Pro Glu Ala Ile Arg Gly Thr Arg 1540 1545 1550	5017
GTT CAG GGC ACC TGG TAT CAA AAG ACG GTA CAG TTG CCT GCG GGT ACT Val Gln Gly Thr Trp Tyr Gln Lys Thr Val Gln Leu Pro Ala Gly Thr 1555 1560 1565	5065
AAG TAT GTT GCT TTC CGT CAC TTC GGC TGT ACG GAC TTC TTC TGG ATC Lys Tyr Val Ala Phe Arg His Phe Gly Cys Thr Asp Phe Phe Trp Ile 1570 1575 1580	5113
AAC CTT GAT GAT GTT GAG ATC AAG GCC AAC GGC AAG CGC GCA GAC TTC Asn Leu Asp Asp Val Glu Ile Lys Ala Asn Gly Lys Arg Ala Asp Phe 1585 1590 1595	5161
ACG GAA ACG TTC GAG TCT TCT ACT CAT GGA GAG GCA CCG GCG GAA TGG Thr Glu Thr Phe Glu Ser Ser Thr His Gly Glu Ala Pro Ala Glu Trp 1600 1605 1610 1615	5209

ACT ACT ATC GAT GCC GAT GGC GAT GGT CAG GGT TGG CTC TGT CTG TCT Thr Thr Ile Asp Ala Asp Gly Asp Gly Gln Gly Trp Leu Cys Leu Ser 1620 1625 1630	5257
TCC GGA CAA TTG GGC TGG CTG ACA GCT CAT GGC GGC ACC AAC GTA GTA Ser Gly Gln Leu Gly Trp Leu Thr Ala His Gly Gly Thr Asn Val Val 1635 1640 1645	5305
GCC TCT TTC TCA TGG AAT GGA ATG GCT TTG AAT CCT GAT AAC TAT CTC Ala Ser Phe Ser Trp Asn Gly Met Ala Leu Asn Pro Asp Asn Tyr Leu 1650 1655 1660	5353
ATC TCA AAG GAT GTT ACA GGC GCA ACT AAG GTA AAG TAC TAC TAT GCA Ile Ser Lys Asp Val Thr Gly Ala Thr Lys Val Lys Tyr Tyr Tyr Ala 1665 1670 1675	5401
GTC AAC GAC GGT TTT CCC GGG GAT CAC TAT GCG GTG ATG ATC TCC AAG Val Asn Asp Gly Phe Pro Gly Asp His Tyr Ala Val Met Ile Ser Lys 1680 1685 1690 1695	5449
ACG GGC ACG AAC GCC GGA GAC TTC ACG GTT GTT TTC GAA GAA ACG CCT Thr Gly Thr Asn Ala Gly Asp Phe Thr Val Val Phe Glu Glu Thr Pro 1700 1705 1710	5497
AAC GGA ATA AAT AAG GGC GGA GCA AGA TTC GGT CTT TCC ACG GAA GCC Asn Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly Leu Ser Thr Glu Ala 1715 1720 1725	5545
GAT GGC GCC AAA CCT CAA AGT GTA TGG ATC GAG CGT ACG GTA GAT TTG Asp Gly Ala Lys Pro Gln Ser Val Trp Ile Glu Arg Thr Val Asp Leu 1730 1735 1740	5593
CCT GCG GGT ACT AAG TAT GTT GCT TTC CGA CAC TAC AAT TGC TCG GAT Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys Ser Asp 1745 1750 1755	5641
TTG AAC TAC ATT CTT TTG GAT GAT ATT CAG TTC ACC ATG GGT GGC AGC Leu Asn Tyr Ile Leu Leu Asp Asp Ile Gln Phe Thr Met Gly Gly Ser 1760 1765 1770 1775	5689
CCC ACC CCG ACC GAT TAT ACC TAC ACG GTG TAT CGT GAC GGT ACG AAG Pro Thr Pro Thr Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Thr Lys 1780 1785 1790	5737
ATC AAG GAA GGT CTG ACC GAA ACG ACC TTC GAA GAA GAC GGT GTA GCT Ile Lys Glu Gly Leu Thr Glu Thr Thr Phe Glu Glu Asp Gly Val Ala 1795 1800 1805	5785
ACG GGC AAC CAT GAG TAT TGC GTG GAA GTG AAG TAC ACA GCC GGC GTA Thr Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly Val 1810 1815 1820	5833
TCT CCG AAA GAG TGT GTA AAC GTA ACT GTT GAT CCT GTG CAG TTC AAT Ser Pro Lys Glu Cys Val Asn Val Thr Val Asp Pro Val Gln Phe Asn 1825 1830 1835	5881
CCT GTA CAG AAC CTG ACC GGT AGT GCA GTC GGC CAG AAA GTA ACG CTT Pro Val Gln Asn Leu Thr Gly Ser Ala Val Gly Gln Lys Val Thr Leu 1840 1845 1850 1855	5929
AAG TGG GAT GCA CCT AAT GGT ACC CCG AAT CCA AAT CCA AAT CCG AAT Lys Trp Asp Ala Pro Asn Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn 1860 1865 1870	5977

CCG GGA ACA ACA ACA CTT TCC GAA TCA TTC GAA AAT GGT ATT CCT GCC Pro Gly Thr Thr Thr Leu Ser Glu Ser Phe Glu Asn Gly Ile Pro Ala 1875 1880 1885	6025
TCA TGG AAG ACG ATC GAT GCA GAC GGT GAC GGC AAC AAT TGG ACG ACG Ser Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Asn Asn Trp Thr Thr 1890 1895 1900	6073
ACC CCT CCT CCC GGA GGC ACC TCT TTT GCA GGT CAC AAC AGT GCG ATC Thr Pro Pro Pro Gly Gly Thr Ser Phe Ala Gly His Asn Ser Ala Ile 1905 1910 1915	6121
TGT GTC TCT TCG GCT TCT TAT ATC AAC TTT GAA GGC CCT CAG AAC CCT Cys Val Ser Ser Ala Ser Tyr Ile Asn Phe Glu Gly Pro Gln Asn Pro 1920 1925 1930 1935	6169
GAT AAC TAT CTG GTT ACA CCG GAG CTA TCT CTT CCT GGC GGA GGA ACG Asp Asn Tyr Leu Val Thr Pro Glu Leu Ser Leu Pro Gly Gly Gly Thr 1940 1945 1950	6217
CTT ACT TTC TGG GTA TGT GCA CAA GAT GCC AAT TAT GCA TCA GAG CAC Leu Thr Phe Trp Val Cys Ala Gln Asp Ala Asn Tyr Ala Ser Glu His 1955 1960 1965	6265
TAT GCC GTG TAT GCA TCT TCT ACG GGT AAC GAC GCT TCC AAC TTC GCC Tyr Ala Val Tyr Ala Ser Ser Thr Gly Asn Asp Ala Ser Asn Phe Ala 1970 1975 1980	6313
AAC GCT TTG TTG GAA GAA GTG CTG ACG GCC AAG ACA GTT GTT ACG GCA Asn Ala Leu Leu Glu Glu Val Leu Thr Ala Lys Thr Val Val Thr Ala 1985 1990 1995	6361
CCT GAA GCC ATT CGT GGC ACT CGT GTT CAG GGC ACC TGG TAT CAA AAG Pro Glu Ala Ile Arg Gly Thr Arg Val Gln Gly Thr Trp Tyr Gln Lys 2000 2005 2010 2015	6409
ACG GTA CAG TTG CCT GCG GGT ACT AAG TAT GTT GCC TTC CGT CAC TTC Thr Val Gln Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Phe 2020 2025 2030	6457
GGC TGT ACG GAC TTC TTC TGG ATC AAC CTT GAT GAA GTT GAG ATC AAG Gly Cys Thr Asp Phe Phe Trp Ile Asn Leu Asp Glu Val Glu Ile Lys 2035 2040 2045	6505
GCC AAC GGC AAG CGC GCA GAC TTC ACG GAA ACG TTC GAG TCT TCT ACT Ala Asn Gly Lys Arg Ala Asp Phe Thr Glu Thr Phe Glu Ser Ser Thr 2050 2055 2060	6553
CAT GGA GAG GCA CCG GCG GAA TGG ACT ACT ATC GAT GCC GAT GGC GAT His Gly Glu Ala Pro Ala Glu Trp Thr Thr Ile Asp Ala Asp Gly Asp 2065 2070 2075	6601
GGT CAG GGT TGG CTC TGT CTG TCT TCC GGA CAA TTG GAC TGG CTG ACA Gly Gln Gly Trp Leu Cys Leu Ser Ser Gly Gln Leu Asp Trp Leu Thr 2080 2085 2090 2095	6649
GCT CAT GGC GGC ACC AAC GTA GTA GCC TCT TTC TCA TGG AAT GGA ATG Ala His Gly Gly Thr Asn Val Val Ala Ser Phe Ser Trp Asn Gly Met 2100 2105 2110	6697
GCT TTG AAT CCT GAT AAC TAT CTC ATC TCA AAG GAT GTT ACA GGC GCA Ala Leu Asn Pro Asp Asn Tyr Leu Ile Ser Lys Asp Val Thr Gly Ala 2115 2120 2125	6745

ACT AAG GTA AAG TAC TAC TAT GCA GTC AAC GAC GGT TTT CCC GGG GAT Thr Lys Val Lys Tyr Tyr Tyr Ala Val Asn Asp Gly Phe Pro Gly Asp 2130 2135 2140	6793
CAC TAT GCG GTG ATG ATC TCC AAG ACG GGC ACG AAC GCC GGA GAC TTC His Tyr Ala Val Met Ile Ser Lys Thr Gly Thr Asn Ala Gly Asp Phe 2145 2150 2155	6841
ACG GTT GTT TTC GAA GAA ACG CCT AAC GGA ATA AAT AAG GGC GGA GCA Thr Val Val Phe Glu Glu Thr Pro Asn Gly Ile Asn Lys Gly Gly Ala 2160 2165 2170 2175	6889
AGA TTC GGT CTT TCC ACG GAA GCC GAT GGC GCC AAA CCT CAA AGT GTA Arg Phe Gly Leu Ser Thr Glu Ala Asp Gly Ala Lys Pro Gln Ser Val 2180 2185 2190	6937
TGG ATC GAG CGT ACG GTA GAT TTG CCT GCG GGC ACG AAG TAT GTT GCT Trp Ile Glu Arg Thr Val Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala 2195 2200 2205	6985
TTC CGT CAC TAC AAT TGC TCG GAT TTG AAC TAC ATT CTT TTG GAT GAT Phe Arg His Tyr Asn Cys Ser Asp Leu Asn Tyr Ile Leu Leu Asp Asp 2210 2215 2220	7033
ATT CAG TTC ACC ATG GGT GGC AGC CCC ACC CCG ACC GAT TAT ACC TAC Ile Gln Phe Thr Met Gly Gly Ser Pro Thr Pro Thr Asp Tyr Thr Tyr 2225 2230 2235	7081
ACG GTG TAT CGT GAC GGT ACG AAG ATC AAG GAA GGT CTG ACC GAA ACG Thr Val Tyr Arg Asp Gly Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr 2240 2245 2250 2255	7129
ACC TTC GAA GAA GAT GGT GTA GCT ACG GGC AAT CAT GAG TAT TGC GTG Thr Phe Glu Glu Asp Gly Val Ala Thr Gly Asn His Glu Tyr Cys Val 2260 2265 2270	7177
GAA GTG AAG TAC ACA GCC GGC GTA TCT CCG AAG GTG TGT GTA AAC GTA Glu Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Val Cys Val Asn Val 2275 2280 2285	7225
ACT ATT AAT CCG ACT CAG TTC AAT CCT GTA CAG AAC CTG ACG GCA GAA Thr Ile Asn Pro Thr Gln Phe Asn Pro Val Gln Asn Leu Thr Ala Glu 2290 2295 2300	7273
CAA GCT CCT AAC AGC ATG GAT GCA ATC CTT AAA TGG AAT GCA CCG GCA Gln Ala Pro Asn Ser Met Asp Ala Ile Leu Lys Trp Asn Ala Pro Ala 2305 2310 2315	7321
TCT AAG CGT GCG GAA GTT CTG AAC GAA GAC TTC GAA AAT GGT ATT CCT Ser Lys Arg Ala Glu Val Leu Asn Glu Asp Phe Glu Asn Gly Ile Pro 2320 2325 2330 2335	7369
TCC TCA TGG AAG ACG ATC GAT GCA GAC GGG GAC GGC AAC AAT TGG ACG Ser Ser Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Asn Asn Trp Thr 2340 2345 2350	7417
ACG ACC CCT CCT CCC GGA GGC TCC TCT TTT GCA GGT CAC AAC AGT GCG Thr Thr Pro Pro Pro Gly Gly Ser Ser Phe Ala Gly His Asn Ser Ala 2355 2360 2365	7465
ATC TGT GTC TCT TCG GCT TCT TAT ATC AAC TTT GAA GGT CCT CAG AAC Ile Cys Val Ser Ser Ala Ser Tyr Ile Asn Phe Glu Gly Pro Gln Asn 2370 2375 2380	7513

CCT GAT AAC TAT CTG GTT ACA CCG GAG CTT TCT CTT CCT GGC GGA GGA Pro Asp Asn Tyr Leu Val Thr Pro Glu Leu Ser Leu Pro Gly Gly Gly 2385 2390 2395	7561
ACG CTT ACT TTC TGG GTA TGT GCA CAA GAT GCC AAT TAT GCA TCA GAG Thr Leu Thr Phe Trp Val Cys Ala Gln Asp Ala Asn Tyr Ala Ser Glu 2400 2405 2410 2415	7609
CAC TAT GCC GTG TAT GCA TCT TCT ACG GGT AAC GAC GCT TCC AAC TTC His Tyr Ala Val Tyr Ala Ser Ser Thr Gly Asn Asp Ala Ser Asn Phe 2420 2425 2430	7657
GCC AAC GCT TTG TTG GAA GAA GTG CTG ACG GCC AAG ACA GTT GTT ACG Ala Asn Ala Leu Leu Glu Glu Val Leu Thr Ala Lys Thr Val Val Thr 2435 2440 2445	7705
GCG CCT GAA GCC ATT CGT GGC ACT CGT GTT CAG GGC ACC TGG TAT CAA Ala Pro Glu Ala Ile Arg Gly Thr Arg Val Gln Gly Thr Trp Tyr Gln 2450 2455 2460	7753
AAG ACG GTA CAG TTG CCT GCG GGT ACT AAG TAT GTT GCC TTC CGT CAC Lys Thr Val Gln Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His 2465 2470 2475	7801
TTC GGC TGT ACG GAC TTC TTC TGG ATC AAC CTT GAT GAT GTT GTA ATC Phe Gly Cys Thr Asp Phe Phe Trp Ile Asn Leu Asp Asp Val Val Ile 2480 2485 2490 2495	7849
ACT TCA GGG AAC GCT CCG TCT TAC ACC TAT ACG ATC TAT CGT AAT AAT Thr Ser Gly Asn Ala Pro Ser Tyr Thr Tyr Thr Ile Tyr Arg Asn Asn 2500 2505 2510	7897
ACA CAG ATA GCA TCA GGC GTA ACG GAG ACT ACT TAC CGA GAT CCG GAC Thr Gln Ile Ala Ser Gly Val Thr Glu Thr Thr Tyr Arg Asp Pro Asp 2515 2520 2525	7945
TTG GCT ACC GGT TTT TAC ACG TAC GGT GTT AAG GTT GTT TAC CCG AAC Leu Ala Thr Gly Phe Tyr Thr Tyr Gly Val Lys Val Val Tyr Pro Asn 2530 2535 2540	7993
GGA GAA TCA GCT ATC GAA ACT GCT ACG TTG AAT ATC ACT TCG TTG GCA Gly Glu Ser Ala Ile Glu Thr Ala Thr Leu Asn Ile Thr Ser Leu Ala 2545 2550 2555	8041
GAC GTA ACG GCT CAG AAG CCT TAC ACG CTG ACA GTT GTA GGA AAG ACG Asp Val Thr Ala Gln Lys Pro Tyr Thr Leu Thr Val Val Gly Lys Thr 2560 2565 2570 2575	8089
ATC ACG GTA ACT TGC CAA GGC GAA GCT ATG ATC TAC GAC ATG AAC GGT Ile Thr Val Thr Cys Gln Gly Glu Ala Met Ile Tyr Asp Met Asn Gly 2580 2585 2590	8137
CGT CGT CTG GCA GCC GGT CGC AAC ACG GTT GTT TAC ACG GCT CAG GGC Arg Arg Leu Ala Ala Gly Arg Asn Thr Val Val Tyr Thr Ala Gln Gly 2595 2600 2605	8185
GGC CAC TAT GCA GTC ATG GTT GTC GTT GAC GGC AAG TCC TAC GTA GAG Gly His Tyr Ala Val Met Val Val Val Asp Gly Lys Ser Tyr Val Glu 2610 2615 2620	8233
AAA CTC GCT GTA AAG TAACGAGATG ATTATTTTCG ATCGGTATGC TCTACCAACC Lys Leu Ala Val Lys 2625	8288

GATCGCTTTA ATCGGTCGCC CGGCTTCCAT AAAAAGGAGT CGGGCGACTC TTTTACTCCA	8348
ACCAAATAAG CATTGTTTTA TAGCCTTTTCG GAATATACTC CGGAAGGGGG TCGAGCTACG	8408
CCCTACAGCG ACTCGGGCTA CGCCGTAGAG CGTACCGAGC TCGCTCTAC GGCTCTTCGA	8468
GCTACGCTGT AGGGCTCACT GCGCCAAGCT CTACGGCTCA GCTCGGCCAC CTCTACGGCT	8528
CCCGGAGCGG AACTCTACGG CTCGGCTCGC TACGCTGTAG AGCGTACCTA CGCCGAGCTC	8588

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2628 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Lys	Leu	Asn	Ser	Leu	Phe	Ser	Leu	Ala	Val	Leu	Leu	Ser	Leu	1	5	10	15
Leu	Cys	Trp	Gly	Gln	Thr	Ala	Ala	Ala	Gln	Gly	Gly	Pro	Lys	Thr	Ala	20	25	30	
Pro	Ser	Val	Thr	His	Gln	Ala	Val	Gln	Lys	Gly	Ile	Arg	Thr	Ser	Lys	35	40	45	
Val	Lys	Asp	Leu	Arg	Asp	Pro	Ile	Pro	Ala	Gly	Met	Ala	Arg	Ile	Ile	50	55	60	
Leu	Glu	Ala	His	Asp	Val	Trp	Glu	Asp	Gly	Thr	Gly	Tyr	Gln	Met	Leu	65	70	75	80
Trp	Asp	Ala	Asp	His	Asn	Gln	Tyr	Gly	Ala	Ser	Ile	Pro	Glu	Glu	Ser	85	90	95	
Phe	Trp	Phe	Ala	Asn	Gly	Thr	Ile	Pro	Ala	Gly	Leu	Tyr	Asp	Pro	Phe	100	105	110	
Glu	Tyr	Lys	Val	Pro	Val	Asn	Ala	Asp	Ala	Ser	Phe	Ser	Pro	Thr	Asn	115	120	125	
Phe	Val	Leu	Asp	Gly	Thr	Ala	Ser	Ala	Asp	Ile	Pro	Ala	Gly	Thr	Tyr	130	135	140	
Asp	Tyr	Val	Ile	Ile	Asn	Pro	Asn	Pro	Gly	Ile	Ile	Tyr	Ile	Val	Gly	145	150	155	160
Glu	Gly	Val	Ser	Lys	Gly	Asn	Asp	Tyr	Val	Val	Glu	Ala	Gly	Lys	Thr	165	170	175	
Tyr	His	Phe	Thr	Val	Gln	Arg	Gln	Gly	Pro	Gly	Asp	Ala	Ala	Ser	Val	180	185	190	
Val	Val	Thr	Gly	Glu	Gly	Gly	Asn	Glu	Phe	Ala	Pro	Val	Gln	Asn	Leu	195	200	205	
Gln	Trp	Ser	Val	Ser	Gly	Gln	Thr	Val	Thr	Leu	Thr	Trp	Gln	Ala	Pro	210	215	220	

94

Ala Ser Asp Lys Arg Thr Tyr Val Leu Asn Glu Ser Phe Asp Thr Gln
 225 230 235 240
 Thr Leu Pro Asn Gly Trp Thr Met Ile Asp Ala Asp Gly Asp Gly His
 245 250 255
 Asn Trp Leu Ser Thr Ile Asn Val Tyr Asn Thr Ala Thr His Thr Gly
 260 265 270
 Asp Gly Ala Met Phe Ser Lys Ser Trp Thr Ala Ser Gly Gly Ala Lys
 275 280 285
 Ile Asp Leu Ser Pro Asp Asn Tyr Leu Val Thr Pro Lys Val Thr Val
 290 295 300
 Pro Glu Asn Gly Lys Leu Ser Tyr Trp Val Ser Ser Gln Val Pro Trp
 305 310 315 320
 Thr Asn Glu His Tyr Gly Val Phe Leu Ser Thr Thr Gly Asn Glu Ala
 325 330 335
 Ala Asn Phe Thr Ile Lys Leu Leu Glu Glu Thr Leu Gly Ser Asp Lys
 340 345 350
 Pro Ala Pro Met Asn Leu Val Lys Ser Glu Gly Val Lys Leu Pro Ala
 355 360 365
 Pro Tyr Gln Glu Arg Thr Ile Asp Leu Ser Ala Tyr Ala Gly Gln Gln
 370 375 380
 Val Tyr Leu Ala Phe Arg His Phe Asn Ser Thr Gly Ile Phe Arg Leu
 385 390 395 400
 Tyr Leu Asp Asp Val Ala Val Ser Gly Glu Gly Ser Ser Asn Asp Tyr
 405 410 415
 Thr Tyr Thr Val Tyr Arg Asp Asn Val Val Ile Ala Gln Asn Leu Ala
 420 425 430
 Ala Thr Thr Phe Asn Gln Glu Asn Val Ala Pro Gly Gln Tyr Asn Tyr
 435 440 445
 Cys Val Glu Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Val Cys Lys
 450 455 460
 Asp Val Thr Val Glu Gly Ser Asn Glu Phe Ala His Val Gln Asn Leu
 465 470 475 480
 Thr Gly Ser Ala Val Gly Gln Lys Val Thr Leu Lys Trp Asp Ala Pro
 485 490 495
 Asn Gly Thr Pro Asn Pro Asn Pro Gly Thr Thr Thr Leu Ser Glu Ser
 500 505 510
 Phe Glu Asn Gly Ile Pro Ala Ser Trp Lys Thr Ile Asp Ala Asp Gly
 515 520 525
 Asp Gly Asn Asn Trp Thr Thr Thr Pro Pro Pro Gly Gly Thr Ser Phe
 530 535 540
 Ala Gly His Asn Ser Ala Ile Cys Ala Ser Ser Ala Ser Tyr Ile Asn
 545 550 555 560

95

Phe Glu Gly Pro Gln Asn Pro Asp Asn Tyr Leu Val Thr Pro Glu Leu
 565 570 575
 Ser Leu Pro Asn Gly Gly Thr Leu Thr Phe Trp Val Cys Ala Gln Asp
 580 585 590
 Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr Ala Ser Ser Thr Gly
 595 600 605
 Asn Asp Ala Ser Asn Phe Ala Asn Ala Leu Leu Glu Glu Val Leu Thr
 610 615 620
 Ala Lys Thr Val Val Thr Ala Pro Glu Ala Ile Arg Gly Thr Arg Val
 625 630 635 640
 Gln Gly Thr Trp Tyr Gln Lys Thr Val Gln Leu Pro Ala Gly Thr Lys
 645 650 655
 Tyr Val Ala Phe Arg His Phe Gly Cys Thr Asp Phe Phe Trp Ile Asn
 660 665 670
 Leu Asp Asp Val Glu Ile Lys Ala Asn Gly Lys Arg Ala Asp Phe Thr
 675 680 685
 Glu Thr Phe Glu Ser Ser Thr His Gly Glu Ala Pro Ala Glu Trp Thr
 690 695 700
 Thr Ile Asp Ala Asp Gly Asp Gly Gln Gly Trp Leu Cys Leu Ser Ser
 705 710 715 720
 Gly Gln Leu Asp Trp Leu Thr Ala His Gly Gly Thr Asn Val Val Ala
 725 730 735
 Ser Phe Ser Trp Asn Gly Met Ala Leu Asn Pro Asp Asn Tyr Leu Ile
 740 745 750
 Ser Lys Asp Val Thr Gly Ala Thr Lys Val Lys Tyr Tyr Tyr Ala Val
 755 760 765
 Asn Asp Gly Phe Pro Gly Asp His Tyr Ala Val Met Ile Ser Lys Thr
 770 775 780
 Gly Thr Asn Ala Gly Asp Phe Thr Val Val Phe Glu Glu Thr Pro Asn
 785 790 795 800
 Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly Leu Ser Thr Glu Ala Asp
 805 810 815
 Gly Ala Lys Pro Gln Ser Val Trp Ile Glu Arg Thr Val Asp Leu Pro
 820 825 830
 Ala Gly Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys Ser Asp Leu
 835 840 845
 Asn Tyr Ile Leu Leu Asp Asp Ile Gln Phe Thr Met Gly Gly Ser Pro
 850 855 860
 Thr Pro Thr Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Thr Lys Ile
 865 870 875 880
 Lys Glu Gly Leu Thr Glu Thr Thr Phe Glu Glu Asp Gly Val Ala Thr
 885 890 895

96

Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly Val Ser
 900 905 910
 Pro Lys Glu Cys Val Asn Val Thr Val Asp Pro Val Gln Phe Asn Pro
 915 920 925
 Val Gln Asn Leu Thr Gly Ser Ala Val Gly Gln Lys Val Thr Leu Lys
 930 935 940
 Trp Asp Ala Pro Asn Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn Pro
 945 950 955 960
 Gly Thr Thr Thr Leu Ser Glu Ser Phe Glu Asn Gly Ile Pro Ala Ser
 965 970 975
 Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Asn Asn Trp Thr Thr Thr
 980 985 990
 Pro Pro Pro Gly Gly Thr Ser Phe Ala Gly His Asn Ser Ala Ile Cys
 995 1000 1005
 Ala Ser Ser Ala Ser Tyr Ile Asn Phe Glu Gly Pro Gln Asn Pro Asp
 1010 1015 1020
 Asn Tyr Leu Val Thr Pro Glu Leu Ser Leu Pro Asn Gly Gly Thr Leu
 1025 1030 1035 1040
 Thr Phe Trp Val Cys Ala Gln Asp Ala Asn Tyr Ala Ser Glu His Tyr
 1045 1050 1055
 Ala Val Tyr Ala Ser Ser Thr Gly Asn Asp Ala Ser Asn Phe Ala Asn
 1060 1065 1070
 Ala Leu Leu Glu Glu Val Leu Thr Ala Lys Thr Val Val Thr Ala Pro
 1075 1080 1085
 Glu Ala Ile Arg Gly Thr Arg Val Gln Gly Thr Trp Tyr Gln Lys Thr
 1090 1095 1100
 Val Gln Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Phe Gly
 1105 1110 1115 1120
 Cys Thr Asp Phe Phe Trp Ile Asn Leu Asp Asp Val Glu Ile Lys Ala
 1125 1130 1135
 Asn Gly Lys Arg Ala Asp Phe Thr Glu Thr Phe Glu Ser Ser Thr His
 1140 1145 1150
 Gly Glu Ala Pro Ala Glu Trp Thr Thr Ile Asp Ala Asp Gly Asp Gly
 1155 1160 1165
 Gln Gly Trp Leu Cys Leu Ser Ser Gly Gln Leu Gly Trp Leu Thr Ala
 1170 1175 1180
 His Gly Gly Thr Asn Val Val Ala Ser Phe Ser Trp Asn Gly Met Ala
 1185 1190 1195 1200
 Leu Asn Pro Asp Asn Tyr Leu Ile Ser Lys Asp Val Thr Gly Ala Thr
 1205 1210 1215
 Lys Val Lys Tyr Tyr Tyr Ala Val Asn Asp Gly Phe Pro Gly Asp His
 1220 1225 1230

Tyr Ala Val Met Ile Ser Lys Thr Gly Thr Asn Ala Gly Asp Phe Thr
 1235 1240 1245
 Val Val Phe Glu Glu Thr Pro Asn Gly Ile Asn Lys Gly Gly Ala Arg
 1250 1255 1260
 Phe Gly Leu Ser Thr Glu Ala Asp Gly Ala Lys Pro Gln Ser Val Trp
 1265 1270 1275 1280
 Ile Glu Arg Thr Val Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe
 1285 1290 1295
 Arg His Tyr Asn Cys Ser Asp Leu Asn Tyr Ile Leu Leu Asp Asp Ile
 1300 1305 1310
 Gln Phe Thr Met Gly Gly Ser Pro Thr Pro Thr Asp Tyr Thr Tyr Thr
 1315 1320 1325
 Val Tyr Arg Asp Gly Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr Thr
 1330 1335 1340
 Phe Glu Glu Asp Gly Val Ala Thr Gly Asn His Glu Tyr Cys Val Glu
 1345 1350 1355 1360
 Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Glu Cys Val Asn Val Thr
 1365 1370 1375
 Val Asp Pro Val Gln Phe Asn Pro Val Gln Asn Leu Thr Gly Ser Ala
 1380 1385 1390
 Val Gly Gln Lys Val Thr Leu Lys Trp Asp Ala Pro Asn Gly Thr Pro
 1395 1400 1405
 Asn Pro Asn Pro Asn Pro Asn Pro Gly Thr Thr Thr Leu Ser Glu Ser
 1410 1415 1420
 Phe Glu Asn Gly Ile Pro Ala Ser Trp Lys Thr Ile Asp Ala Asp Gly
 1425 1430 1435 1440
 Asp Gly Asn Asn Trp Thr Thr Thr Pro Pro Pro Gly Gly Thr Ser Phe
 1445 1450 1455
 Ala Gly His Asn Ser Ala Ile Cys Ala Ser Ser Ala Ser Tyr Ile Asn
 1460 1465 1470
 Phe Glu Gly Pro Gln Asn Pro Asp Asn Tyr Leu Val Thr Pro Glu Leu
 1475 1480 1485
 Ser Leu Pro Asn Gly Gly Thr Leu Thr Phe Trp Val Cys Ala Gln Asp
 1490 1495 1500
 Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr Ala Ser Ser Thr Gly
 1505 1510 1515 1520
 Asn Asp Ala Ser Asn Phe Ala Asn Ala Leu Leu Glu Glu Val Leu Thr
 1525 1530 1535
 Ala Lys Thr Val Val Thr Ala Pro Glu Ala Ile Arg Gly Thr Arg Val
 1540 1545 1550
 Gln Gly Thr Trp Tyr Gln Lys Thr Val Gln Leu Pro Ala Gly Thr Lys
 1555 1560 1565

Tyr Val Ala Phe Arg His Phe Gly Cys Thr Asp Phe Phe Trp Ile Asn
 1570 1575 1580
 Leu Asp Asp Val Glu Ile Lys Ala Asn Gly Lys Arg Ala Asp Phe Thr
 1585 1590 1595 1600
 Glu Thr Phe Glu Ser Ser Thr His Gly Glu Ala Pro Ala Glu Trp Thr
 1605 1610 1615
 Thr Ile Asp Ala Asp Gly Asp Gly Gln Gly Trp Leu Cys Leu Ser Ser
 1620 1625 1630
 Gly Gln Leu Gly Trp Leu Thr Ala His Gly Gly Thr Asn Val Val Ala
 1635 1640 1645
 Ser Phe Ser Trp Asn Gly Met Ala Leu Asn Pro Asp Asn Tyr Leu Ile
 1650 1655 1660
 Ser Lys Asp Val Thr Gly Ala Thr Lys Val Lys Tyr Tyr Tyr Ala Val
 1665 1670 1675 1680
 Asn Asp Gly Phe Pro Gly Asp His Tyr Ala Val Met Ile Ser Lys Thr
 1685 1690 1695
 Gly Thr Asn Ala Gly Asp Phe Thr Val Val Phe Glu Glu Thr Pro Asn
 1700 1705 1710
 Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly Leu Ser Thr Glu Ala Asp
 1715 1720 1725
 Gly Ala Lys Pro Gln Ser Val Trp Ile Glu Arg Thr Val Asp Leu Pro
 1730 1735 1740
 Ala Gly Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys Ser Asp Leu
 1745 1750 1755 1760
 Asn Tyr Ile Leu Leu Asp Asp Ile Gln Phe Thr Met Gly Gly Ser Pro
 1765 1770 1775
 Thr Pro Thr Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Thr Lys Ile
 1780 1785 1790
 Lys Glu Gly Leu Thr Glu Thr Thr Phe Glu Glu Asp Gly Val Ala Thr
 1795 1800 1805
 Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly Val Ser
 1810 1815 1820
 Pro Lys Glu Cys Val Asn Val Thr Val Asp Pro Val Gln Phe Asn Pro
 1825 1830 1835 1840
 Val Gln Asn Leu Thr Gly Ser Ala Val Gly Gln Lys Val Thr Leu Lys
 1845 1850 1855
 Trp Asp Ala Pro Asn Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn Pro
 1860 1865 1870
 Gly Thr Thr Thr Leu Ser Glu Ser Phe Glu Asn Gly Ile Pro Ala Ser
 1875 1880 1885
 Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Asn Asn Trp Thr Thr Thr
 1890 1895 1900

Pro Pro Pro Gly Gly Thr Ser Phe Ala Gly His Asn Ser Ala Ile Cys
 1905 1910 1915 1920
 Val Ser Ser Ala Ser Tyr Ile Asn Phe Glu Gly Pro Gln Asn Pro Asp
 1925 1930 1935
 Asn Tyr Leu Val Thr Pro Glu Leu Ser Leu Pro Gly Gly Gly Thr Leu
 1940 1945 1950
 Thr Phe Trp Val Cys Ala Gln Asp Ala Asn Tyr Ala Ser Glu His Tyr
 1955 1960 1965
 Ala Val Tyr Ala Ser Ser Thr Gly Asn Asp Ala Ser Asn Phe Ala Asn
 1970 1975 1980
 Ala Leu Leu Glu Glu Val Leu Thr Ala Lys Thr Val Val Thr Ala Pro
 1985 1990 1995 2000
 Glu Ala Ile Arg Gly Thr Arg Val Gln Gly Thr Trp Tyr Gln Lys Thr
 2005 2010 2015
 Val Gln Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Phe Gly
 2020 2025 2030
 Cys Thr Asp Phe Phe Trp Ile Asn Leu Asp Glu Val Glu Ile Lys Ala
 2035 2040 2045
 Asn Gly Lys Arg Ala Asp Phe Thr Glu Thr Phe Glu Ser Ser Thr His
 2050 2055 2060
 Gly Glu Ala Pro Ala Glu Trp Thr Thr Ile Asp Ala Asp Gly Asp Gly
 2065 2070 2075 2080
 Gln Gly Trp Leu Cys Leu Ser Ser Gly Gln Leu Asp Trp Leu Thr Ala
 2085 2090 2095
 His Gly Gly Thr Asn Val Val Ala Ser Phe Ser Trp Asn Gly Met Ala
 2100 2105 2110
 Leu Asn Pro Asp Asn Tyr Leu Ile Ser Lys Asp Val Thr Gly Ala Thr
 2115 2120 2125
 Lys Val Lys Tyr Tyr Tyr Ala Val Asn Asp Gly Phe Pro Gly Asp His
 2130 2135 2140
 Tyr Ala Val Met Ile Ser Lys Thr Gly Thr Asn Ala Gly Asp Phe Thr
 2145 2150 2155 2160
 Val Val Phe Glu Glu Thr Pro Asn Gly Ile Asn Lys Gly Gly Ala Arg
 2165 2170 2175
 Phe Gly Leu Ser Thr Glu Ala Asp Gly Ala Lys Pro Gln Ser Val Trp
 2180 2185 2190
 Ile Glu Arg Thr Val Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe
 2195 2200 2205
 Arg His Tyr Asn Cys Ser Asp Leu Asn Tyr Ile Leu Leu Asp Asp Ile
 2210 2215 2220
 Gln Phe Thr Met Gly Gly Ser Pro Thr Pro Thr Asp Tyr Thr Tyr Thr
 2225 2230 2235 2240

100

Val Tyr Arg Asp Gly Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr Thr
 2245 2250 2255
 Phe Glu Glu Asp Gly Val Ala Thr Gly Asn His Glu Tyr Cys Val Glu
 2260 2265 2270
 Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Val Cys Val Asn Val Thr
 2275 2280 2285
 Ile Asn Pro Thr Gln Phe Asn Pro Val Gln Asn Leu Thr Ala Glu Gln
 2290 2295 2300
 Ala Pro Asn Ser Met Asp Ala Ile Leu Lys Trp Asn Ala Pro Ala Ser
 2305 2310 2315 2320
 Lys Arg Ala Glu Val Leu Asn Glu Asp Phe Glu Asn Gly Ile Pro Ser
 2325 2330 2335
 Ser Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Asn Asn Trp Thr Thr
 2340 2345 2350
 Thr Pro Pro Pro Gly Gly Ser Ser Phe Ala Gly His Asn Ser Ala Ile
 2355 2360 2365
 Cys Val Ser Ser Ala Ser Tyr Ile Asn Phe Glu Gly Pro Gln Asn Pro
 2370 2375 2380
 Asp Asn Tyr Leu Val Thr Pro Glu Leu Ser Leu Pro Gly Gly Gly Thr
 2385 2390 2395 2400
 Leu Thr Phe Trp Val Cys Ala Gln Asp Ala Asn Tyr Ala Ser Glu His
 2405 2410 2415
 Tyr Ala Val Tyr Ala Ser Ser Thr Gly Asn Asp Ala Ser Asn Phe Ala
 2420 2425 2430
 Asn Ala Leu Leu Glu Glu Val Leu Thr Ala Lys Thr Val Val Thr Ala
 2435 2440 2445
 Pro Glu Ala Ile Arg Gly Thr Arg Val Gln Gly Thr Trp Tyr Gln Lys
 2450 2455 2460
 Thr Val Gln Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Phe
 2465 2470 2475 2480
 Gly Cys Thr Asp Phe Phe Trp Ile Asn Leu Asp Asp Val Val Ile Thr
 2485 2490 2495
 Ser Gly Asn Ala Pro Ser Tyr Thr Tyr Thr Ile Tyr Arg Asn Asn Thr
 2500 2505 2510
 Gln Ile Ala Ser Gly Val Thr Glu Thr Thr Tyr Arg Asp Pro Asp Leu
 2515 2520 2525
 Ala Thr Gly Phe Tyr Thr Tyr Gly Val Lys Val Val Tyr Pro Asn Gly
 2530 2535 2540
 Glu Ser Ala Ile Glu Thr Ala Thr Leu Asn Ile Thr Ser Leu Ala Asp
 2545 2550 2555 2560
 Val Thr Ala Gln Lys Pro Tyr Thr Leu Thr Val Val Gly Lys Thr Ile
 2565 2570 2575

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Thr Val Thr Cys Gln Gly Glu Ala Met Ile Tyr Asp Met Asn Gly Arg
 2580 2585 2590

Arg Leu Ala Ala Gly Arg Asn Thr Val Val Tyr Thr Ala Gln Gly Gly
 2595 2600 2605

His Tyr Ala Val Met Val Val Val Asp Gly Lys Ser Tyr Val Glu Lys
 2610 2615 2620

Leu Ala Val Lys
 2625

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCG AAT CCG AAT CCC GGA ACA ACA ACA CTT TCC GAA TCA TTC GAA AAT Pro Asn Pro Asn Pro Gly Thr Thr Thr Leu Ser Glu Ser Phe Glu Asn 2630 2635 2640	48
GGT ATT CCT GCC TCA TGG AAG ACG ATC GAT GCA GAC GGT GAC GGC AAC Gly Ile Pro Ala Ser Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Asn 2645 2650 2655 2660	96
AAT TGG ACG ACG ACC CCT CCT CCC GGA GGC ACC TCT TTT GCA GGT CAC Asn Trp Thr Thr Thr Pro Pro Pro Gly Gly Thr Ser Phe Ala Gly His 2665 2670 2675	144
AAC AGT GCA ATC TGT GCC TCT TCG GCT TCT TAT ATC AAC TTT GAA GGT Asn Ser Ala Ile Cys Ala Ser Ser Ala Ser Tyr Ile Asn Phe Glu Gly 2680 2685 2690	192
CCT CAG AAC CCT GAT AAC TAT CTG GTT ACA CCG GAG CTA TCT CTT CCT Pro Gln Asn Pro Asp Asn Tyr Leu Val Thr Pro Glu Leu Ser Leu Pro 2695 2700 2705	240
AAC GGA GGA ACG CTT ACT TTC TGG GTA TGT GCA CAA GAT GCC AAT TAT Asn Gly Gly Thr Leu Thr Phe Trp Val Cys Ala Gln Asp Ala Asn Tyr 2710 2715 2720	288
GCA TCA GAG CAC TAT GCC GTG TAC GCA TCT TCT ACG GGT AAC GAC GCT Ala Ser Glu His Tyr Ala Val Tyr Ala Ser Ser Thr Gly Asn Asp Ala 2725 2730 2735 2740	336
TCC AAC TTC GCC AAC GCT TTG TTG GAA GAA GTG CTG ACG GCC AAG ACA Ser Asn Phe Ala Asn Ala Leu Leu Glu Glu Val Leu Thr Ala Lys Thr 2745 2750 2755	384

GTT GTT ACG GCA CCT GAA GCC ATT CGT GGC ACT CGT GTT CAG GGC ACC Val Val Thr Ala Pro Glu Ala Ile Arg Gly Thr Arg Val Gln Gly Thr 2760 2765 2770	432
TGG TAT CAA AAG ACG GTA CAG TTG CCT GCG GGT ACT AAG TAT GTT GCT Trp Tyr Gln Lys Thr Val Gln Leu Pro Ala Gly Thr Lys Tyr Val Ala 2775 2780 2785	480
TTC CGT CAC TTC GGC TGT ACG GAC TTC TTC TGG ATT AAC CTT GAT GAT Phe Arg His Phe Gly Cys Thr Asp Phe Phe Trp Ile Asn Leu Asp Asp 2790 2795 2800	528
GTT GAG ATC AAG GCC AAC GGC AAG CGC GCA GAC TTC ACG GAA ACG TTC Val Glu Ile Lys Ala Asn Gly Lys Arg Ala Asp Phe Thr Glu Thr Phe 2805 2810 2815 2820	576
GAG TCT TCT ACT CAT GGA GAG GCA CCG GCG GAA TGG ACT ACT ATC GAT Glu Ser Ser Thr His Gly Glu Ala Pro Ala Glu Trp Thr Thr Ile Asp 2825 2830 2835	624
GCC GAT GGC GAT GGT CAG GGT TGG CTC TGT CTG TCT TCC GGA CAA TTG Ala Asp Gly Asp Gly Gln Gly Trp Leu Cys Leu Ser Ser Gly Gln Leu 2840 2845 2850	672
GAC TGG CTG ACA GCT CAT GGC GGC ACC AAC GTA GTA GCC TCT TTC TCA Asp Trp Leu Thr Ala His Gly Gly Thr Asn Val Val Ala Ser Phe Ser 2855 2860 2865	720
TGG AAT GGA ATG GCT TTG AAT CCT GAT AAC TAT CTC ATC TCA AAG GAT Trp Asn Gly Met Ala Leu Asn Pro Asp Asn Tyr Leu Ile Ser Lys Asp 2870 2875 2880	768
GTT ACA GGC GCA ACT AAG GTA AAG TAC TAC TAT GCA GTC AAC GAC GGT Val Thr Gly Ala Thr Lys Val Lys Tyr Tyr Tyr Ala Val Asn Asp Gly 2885 2890 2895 2900	816
TTT CCC GGG GAT CAC TAT GCG GTG ATG ATC TCC AAG ACG GGC ACG AAC Phe Pro Gly Asp His Tyr Ala Val Met Ile Ser Lys Thr Gly Thr Asn 2905 2910 2915	864
GCC GGA GAC TTC ACG GTT GTT TTC GAA GAA ACG CCT AAC GGA ATA AAT Ala Gly Asp Phe Thr Val Val Phe Glu Glu Thr Pro Asn Gly Ile Asn 2920 2925 2930	912
AAG GGC GGA GCA AGA TTC GGT CTT TCC ACG GAA GCC GAT GGC GCC AAA Lys Gly Gly Ala Arg Phe Gly Leu Ser Thr Glu Ala Asp Gly Ala Lys 2935 2940 2945	960
CCT CAA AGT GTA TGG ATC GAG CGT ACG GTA GAT TTG CCT GCG GGT ACT Pro Gln Ser Val Trp Ile Glu Arg Thr Val Asp Leu Pro Ala Gly Thr 2950 2955 2960	1008
AAG TAT GTT GCT TTC CGT CAC TAC AAT TGC TCG GAT TTG AAC TAC ATT Lys Tyr Val Ala Phe Arg His Tyr Asn Cys Ser Asp Leu Asn Tyr Ile 2965 2970 2975 2980	1056
CTT TTG GAT GAT ATT CAG TTC ACC ATG GGT GGC AGC CCC ACC CCG ACC Leu Leu Asp Asp Ile Gln Phe Thr Met Gly Gly Ser Pro Thr Pro Thr 2985 2990 2995	1104
GAT TAT ACC TAC ACG GTG TAT CGT GAC GGT ACG AAG ATC AAG GAA GGT Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Thr Lys Ile Lys Glu Gly 3000 3005 3010	1152

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CTG ACC GAA ACG ACC TTC GAA GAA GAC GGT GTA GCT ACG GGC AAC CAT	1200
Leu Thr Glu Thr Thr Phe Glu Glu Asp Gly Val Ala Thr Gly Asn His	
3015 3020 3025	
GAG TAT TGC GTG GAA GTG AAG TAC ACA GCC GGC GTA TCT CCG AAA GAG	1248
Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Glu	
3030 3035 3040	
TGT GTA AAC GTA ACT GTT GAT CCT GTG CAG TTC AAT CCT GTA CAG AAC	1296
Cys Val Asn Val Thr Val Asp Pro Val Gln Phe Asn Pro Val Gln Asn	
3045 3050 3055 3060	
CTG ACC GGT AGT GCA GTC GGC CAG AAA GTA ACG CTT AAG TGG GAT GCA	1344
Leu Thr Gly Ser Ala Val Gly Gln Lys Val Thr Leu Lys Trp Asp Ala	
3065 3070 3075	
CCT AAT	1350
Pro Asn	

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Pro Asn Pro Asn Pro Gly Thr Thr Thr Leu Ser Glu Ser Phe Glu Asn	
1 5 10 15	
Gly Ile Pro Ala Ser Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Asn	
20 25 30	
Asn Trp Thr Thr Thr Pro Pro Pro Gly Gly Thr Ser Phe Ala Gly His	
35 40 45	
Asn Ser Ala Ile Cys Ala Ser Ser Ala Ser Tyr Ile Asn Phe Glu Gly	
50 55 60	
Pro Gln Asn Pro Asp Asn Tyr Leu Val Thr Pro Glu Leu Ser Leu Pro	
65 70 75 80	
Asn Gly Gly Thr Leu Thr Phe Trp Val Cys Ala Gln Asp Ala Asn Tyr	
85 90 95	
Ala Ser Glu His Tyr Ala Val Tyr Ala Ser Ser Thr Gly Asn Asp Ala	
100 105 110	
Ser Asn Phe Ala Asn Ala Leu Leu Glu Glu Val Leu Thr Ala Lys Thr	
115 120 125	
Val Val Thr Ala Pro Glu Ala Ile Arg Gly Thr Arg Val Gln Gly Thr	
130 135 140	
Trp Tyr Gln Lys Thr Val Gln Leu Pro Ala Gly Thr Lys Tyr Val Ala	
145 150 155 160	

[illegible]

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1368 base pairs
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGT ACC CCG AAT CCA AAT CCA AAT CCG AAT CCG GGA ACA ACA ACA CTT	48
Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn Pro Gly Thr Thr Thr Leu	
455 460 465	
TCC GAA TCA TTC GAA AAT GGT ATT CCT GCC TCA TGG AAG ACG ATC GAT	96
Ser Glu Ser Phe Glu Asn Gly Ile Pro Ala Ser Trp Lys Thr Ile Asp	
470 475 480	
GCA GAC GGT GAC GGC AAC AAT TGG ACG ACG ACC CCT CCT CCC GGA GGC	144
Ala Asp Gly Asp Gly Asn Asn Trp Thr Thr Thr Pro Pro Pro Gly Gly	
485 490 495	
ACC TCT TTT GCA GGT CAC AAC AGT GCG ATC TGT GCC TCT TCG GCT TCT	192
Thr Ser Phe Ala Gly His Asn Ser Ala Ile Cys Ala Ser Ser Ala Ser	
500 505 510	
TAT ATC AAC TTT GAA GGC CCT CAG AAC CCT GAT AAC TAT CTG GTT ACA	240
Tyr Ile Asn Phe Glu Gly Pro Gln Asn Pro Asp Asn Tyr Leu Val Thr	
515 520 525 530	
CCG GAG CTA TCT CTT CCT AAC GGA GGA ACG CTT ACT TTC TGG GTA TGT	288
Pro Glu Leu Ser Leu Pro Asn Gly Gly Thr Leu Thr Phe Trp Val Cys	
535 540 545	
GCA CAA GAT GCC AAT TAT GCA TCA GAG CAC TAT GCC GTG TAT GCA TCT	336
Ala Gln Asp Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr Ala Ser	
550 555 560	
TCT ACG GGT AAC GAC GCT TCC AAC TTC GCC AAC GCT TTG TTG GAA GAA	384
Ser Thr Gly Asn Asp Ala Ser Asn Phe Ala Asn Ala Leu Leu Glu Glu	
565 570 575	
GTG CTG ACG GCC AAG ACA GTT GTT ACG GCA CCT GAA GCC ATT CGT GGC	432
Val Leu Thr Ala Lys Thr Val Val Thr Ala Pro Glu Ala Ile Arg Gly	
580 585 590	
ACT CGT GTT CAG GGC ACC TGG TAT CAA AAG ACG GTA CAG TTG CCT GCG	480
Thr Arg Val Gln Gly Thr Trp Tyr Gln Lys Thr Val Gln Leu Pro Ala	
595 600 605 610	
GGT ACT AAG TAT GTT GCT TTC CGT CAC TTC GGC TGT ACG GAC TTC TTC	528
Gly Thr Lys Tyr Val Ala Phe Arg His Phe Gly Cys Thr Asp Phe Phe	
615 620 625	
TGG ATC AAC CTT GAT GAT GTT GAG ATC AAG GCC AAC GGC AAG CGC GCA	576
Trp Ile Asn Leu Asp Asp Val Glu Ile Lys Ala Asn Gly Lys Arg Ala	
630 635 640	
GAC TTC ACG GAA ACG TTC GAG TCT TCT ACT CAT GGA GAG GCA CCG GCG	624
Asp Phe Thr Glu Thr Phe Glu Ser Ser Thr His Gly Glu Ala Pro Ala	
645 650 655	

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GAA TGG ACT ACT ATC GAT GCC GAT GGC GAT GGT CAG GGT TGG CTC TGT Glu Trp Thr Thr Ile Asp Ala Asp Gly Asp Gly Gln Gly Trp Leu Cys 660 665 670	672
CTG TCT TCC GGA CAA TTG GGC TGG CTG ACA GCT CAT GGC GGC ACC AAC Leu Ser Ser Gly Gln Leu Gly Trp Leu Thr Ala His Gly Gly Thr Asn 675 680 685 690	720
GTA GTA GCC TCT TTC TCA TGG AAT GGA ATG GCT TTG AAT CCT GAT AAC Val Val Ala Ser Phe Ser Trp Asn Gly Met Ala Leu Asn Pro Asp Asn 695 700 705	768
TAT CTC ATC TCA AAG GAT GTT ACA GGC GCA ACT AAG GTA AAG TAC TAC Tyr Leu Ile Ser Lys Asp Val Thr Gly Ala Thr Lys Val Lys Tyr Tyr 710 715 720	816
TAT GCA GTC AAC GAC GGT TTT CCC GGG GAT CAC TAT GCG GTG ATG ATC Tyr Ala Val Asn Asp Gly Phe Pro Gly Asp His Tyr Ala Val Met Ile 725 730 735	864
TCC AAG ACG GGC ACG AAC GCC GGA GAC TTC ACG GTT GTT TTC GAA GAA Ser Lys Thr Gly Thr Asn Ala Gly Asp Phe Thr Val Val Phe Glu Glu 740 745 750	912
ACG CCT AAC GGA ATA AAT AAG GGC GGA GCA AGA TTC GGT CTT TCC ACG Thr Pro Asn Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly Leu Ser Thr 755 760 765 770	960
GAA GCC GAT GGC GCC AAA CCT CAA AGT GTA TGG ATC GAG CGT ACG GTA Glu Ala Asp Gly Ala Lys Pro Gln Ser Val Trp Ile Glu Arg Thr Val 775 780 785	1008
GAT TTG CCT GCG GGT ACT AAG TAT GTT GCT TTC CGT CAC TAC AAT TGC Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys 790 795 800	1056
TCG GAT TTG AAC TAC ATT CTT TTG GAT GAT ATT CAG TTC ACC ATG GGT Ser Asp Leu Asn Tyr Ile Leu Leu Asp Asp Ile Gln Phe Thr Met Gly 805 810 815	1104
GGC AGC CCC ACC CCG ACC GAT TAT ACC TAC ACG GTG TAT CGT GAC GGT Gly Ser Pro Thr Pro Thr Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly 820 825 830	1152
ACG AAG ATC AAG GAA GGT CTG ACC GAA ACG ACC TTC GAA GAA GAC GGT Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr Thr Phe Glu Glu Asp Gly 835 840 845 850	1200
GTA GCT ACG GGC AAC CAT GAG TAT TGC GTG GAA GTG AAG TAC ACA GCC Val Ala Thr Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala 855 860 865	1248
GGC GTA TCT CCG AAA GAG TGT GTA AAC GTA ACT GTT GAT CCT GTG CAG Gly Val Ser Pro Lys Glu Cys Val Asn Val Thr Val Asp Pro Val Gln 870 875 880	1296
TTC AAT CCT GTA CAG AAC CTG ACC GGT AGT GCA GTC GGC CAG AAA GTA Phe Asn Pro Val Gln Asn Leu Thr Gly Ser Ala Val Gly Gln Lys Val 885 890 895	1344
ACG CTT AAG TGG GAT GCA CCT AAT Thr Leu Lys Trp Asp Ala Pro Asn 900 905	1368

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 456 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn Pro Gly Thr Thr Thr Leu
 1 5 10 15
 Ser Glu Ser Phe Glu Asn Gly Ile Pro Ala Ser Trp Lys Thr Ile Asp
 20 25 30
 Ala Asp Gly Asp Gly Asn Asn Trp Thr Thr Thr Pro Pro Pro Gly Gly
 35 40 45
 Thr Ser Phe Ala Gly His Asn Ser Ala Ile Cys Ala Ser Ser Ala Ser
 50 55 60
 Tyr Ile Asn Phe Glu Gly Pro Gln Asn Pro Asp Asn Tyr Leu Val Thr
 65 70 75 80
 Pro Glu Leu Ser Leu Pro Asn Gly Gly Thr Leu Thr Phe Trp Val Cys
 85 90 95
 Ala Gln Asp Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr Ala Ser
 100 105 110
 Ser Thr Gly Asn Asp Ala Ser Asn Phe Ala Asn Ala Leu Leu Glu Glu
 115 120 125
 Val Leu Thr Ala Lys Thr Val Val Thr Ala Pro Glu Ala Ile Arg Gly
 130 135 140
 Thr Arg Val Gln Gly Thr Trp Tyr Gln Lys Thr Val Gln Leu Pro Ala
 145 150 155 160
 Gly Thr Lys Tyr Val Ala Phe Arg His Phe Gly Cys Thr Asp Phe Phe
 165 170 175
 Trp Ile Asn Leu Asp Asp Val Glu Ile Lys Ala Asn Gly Lys Arg Ala
 180 185 190
 Asp Phe Thr Glu Thr Phe Glu Ser Ser Thr His Gly Glu Ala Pro Ala
 195 200 205
 Glu Trp Thr Thr Ile Asp Ala Asp Gly Asp Gly Gln Gly Trp Leu Cys
 210 215 220
 Leu Ser Ser Gly Gln Leu Gly Trp Leu Thr Ala His Gly Gly Thr Asn
 225 230 235 240
 Val Val Ala Ser Phe Ser Trp Asn Gly Met Ala Leu Asn Pro Asp Asn
 245 250 255
 Tyr Leu Ile Ser Lys Asp Val Thr Gly Ala Thr Lys Val Lys Tyr Tyr
 260 265 270

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Tyr Ala Val Asn Asp Gly Phe Pro Gly Asp His Tyr Ala Val Met Ile
 275 280 285
 Ser Lys Thr Gly Thr Asn Ala Gly Asp Phe Thr Val Val Phe Glu Glu
 290 295 300
 Thr Pro Asn Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly Leu Ser Thr
 305 310 315 320
 Glu Ala Asp Gly Ala Lys Pro Gln Ser Val Trp Ile Glu Arg Thr Val
 325 330 335
 Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys
 340 345 350
 Ser Asp Leu Asn Tyr Ile Leu Leu Asp Asp Ile Gln Phe Thr Met Gly
 355 360 365
 Gly Ser Pro Thr Pro Thr Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly
 370 375 380
 Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr Thr Phe Glu Glu Asp Gly
 385 390 395 400
 Val Ala Thr Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala
 405 410 415
 Gly Val Ser Pro Lys Glu Cys Val Asn Val Thr Val Asp Pro Val Gln
 420 425 430
 Phe Asn Pro Val Gln Asn Leu Thr Gly Ser Ala Val Gly Gln Lys Val
 435 440 445
 Thr Leu Lys Trp Asp Ala Pro Asn
 450 455

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGT ACC CCG AAT CCA AAT CCA AAT CCG AAT CCG GGA ACA ACA ACA CTT	48
Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn Pro Gly Thr Thr Thr Leu	
460 465 470	
TCC GAA TCA TTC GAA AAT GGT ATT CCT GCC TCA TGG AAG ACG ATC GAT	96
Ser Glu Ser Phe Glu Asn Gly Ile Pro Ala Ser Trp Lys Thr Ile Asp	
475 480 485	

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GCA GAC GGT GAC GGC AAC AAT TGG ACG ACG ACC CCT CCT CCC GGA GGC Ala Asp Gly Asp Gly Asn Asn Trp Thr Thr Thr Pro Pro Gly Gly 490 495 500	144
ACC TCT TTT GCA GGT CAC AAC AGT GCG ATC TGT GCC TCT TCG GCT TCT Thr Ser Phe Ala Gly His Asn Ser Ala Ile Cys Ala Ser Ser Ala Ser 505 510 515 520	192
TAT ATC AAC TTT GAA GGC CCT CAG AAC CCT GAT AAC TAT CTG GTT ACA Tyr Ile Asn Phe Glu Gly Pro Gln Asn Pro Asp Asn Tyr Leu Val Thr 525 530 535	240
CCG GAG CTA TCT CTT CCT AAC GGA GGA ACG CTT ACT TTC TGG GTA TGT Pro Glu Leu Ser Leu Pro Asn Gly Gly Thr Leu Thr Phe Trp Val Cys 540 545 550	288
GCA CAA GAT GCC AAT TAT GCA TCA GAG CAC TAT GCC GTG TAT GCA TCT Ala Gln Asp Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr Ala Ser 555 560 565	336
TCT ACG GGT AAC GAC GCT TCC AAC TTC GCC AAC GCT TTG TTG GAA GAA Ser Thr Gly Asn Asp Ala Ser Asn Phe Ala Asn Ala Leu Leu Glu Glu 570 575 580	384
GTG CTG ACG GCC AAG ACA GTT GTT ACG GCA CCT GAA GCC ATT CGT GGC Val Leu Thr Ala Lys Thr Val Val Thr Ala Pro Glu Ala Ile Arg Gly 585 590 595 600	432
ACT CGT GTT CAG GGC ACC TGG TAT CAA AAG ACG GTA CAG TTG CCT GCG Thr Arg Val Gln Gly Thr Trp Tyr Gln Lys Thr Val Gln Leu Pro Ala 605 610 615	480
GGT ACT AAG TAT GTT GCT TTC CGT CAC TTC GGC TGT ACG GAC TTC TTC Gly Thr Lys Tyr Val Ala Phe Arg His Phe Gly Cys Thr Asp Phe Phe 620 625 630	528
TGG ATC AAC CTT GAT GAT GTT GAG ATC AAG GCC AAC GGC AAG CGC GCA Trp Ile Asn Leu Asp Asp Val Glu Ile Lys Ala Asn Gly Lys Arg Ala 635 640 645	576
GAC TTC ACG GAA ACG TTC GAG TCT TCT ACT CAT GGA GAG GCA CCG GCG Asp Phe Thr Glu Thr Phe Glu Ser Ser Thr His Gly Glu Ala Pro Ala 650 655 660	624
GAA TGG ACT ACT ATC GAT GCC GAT GGC GAT GGT CAG GGT TGG CTC TGT Glu Trp Thr Thr Ile Asp Ala Asp Gly Asp Gly Gln Gly Trp Leu Cys 665 670 675 680	672
CTG TCT TCC GGA CAA TTG GGC TGG CTG ACA GCT CAT GGC GGC ACC AAC Leu Ser Ser Gly Gln Leu Gly Trp Leu Thr Ala His Gly Gly Thr Asn 685 690 695	720
GTA GTA GCC TCT TTC TCA TGG AAT GGA ATG GCT TTG AAT CCT GAT AAC Val Val Ala Ser Phe Ser Trp Asn Gly Met Ala Leu Asn Pro Asp Asn 700 705 710	768
TAT CTC ATC TCA AAG GAT GTT ACA GGC GCA ACT AAG GTA AAG TAC TAC Tyr Leu Ile Ser Lys Asp Val Thr Gly Ala Thr Lys Val Lys Tyr Tyr 715 720 725	816
TAT GCA GTC AAC GAC GGT TTT CCC GGG GAT CAC TAT GCG GTG ATG ATC Tyr Ala Val Asn Asp Gly Phe Pro Gly Asp His Tyr Ala Val Met Ile 730 735 740	864

110

TCC AAG ACG GGC ACG AAC GCC GGA GAC TTC ACG GTT GTT TTC GAA GAA Ser Lys Thr Gly Thr Asn Ala Gly Asp Phe Thr Val Val Phe Glu Glu 745 750 755 760	912
ACG CCT AAC GGA ATA AAT AAG GGC GGA GCA AGA TTC GGT CTT TCC ACG Thr Pro Asn Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly Leu Ser Thr 765 770 775	960
GAA GCC GAT GGC GCC AAA CCT CAA AGT GTA TGG ATC GAG CGT ACG GTA Glu Ala Asp Gly Ala Lys Pro Gln Ser Val Trp Ile Glu Arg Thr Val 780 785 790	1008
GAT TTG CCT GCG GGT ACT AAG TAT GTT GCT TTC CGA CAC TAC AAT TGC Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys 795 800 805	1056
TCG GAT TTG AAC TAC ATT CTT TTG GAT GAT ATT CAG TTC ACC ATG GGT Ser Asp Leu Asn Tyr Ile Leu Leu Asp Asp Ile Gln Phe Thr Met Gly 810 815 820	1104
GGC AGC CCC ACC CCG ACC GAT TAT ACC TAC ACG GTG TAT CGT GAC GGT Gly Ser Pro Thr Pro Thr Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly 825 830 835 840	1152
ACG AAG ATC AAG GAA GGT CTG ACC GAA ACG ACC TTC GAA GAA GAC GGT Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr Thr Phe Glu Glu Asp Gly 845 850 855	1200
GTA GCT ACG GGC AAC CAT GAG TAT TGC GTG GAA GTG AAG TAC ACA GCC Val Ala Thr Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala 860 865 870	1248
GGC GTA TCT CCG AAA GAG TGT GTA AAC GTA ACT GTT GAT CCT GTG CAG Gly Val Ser Pro Lys Glu Cys Val Asn Val Thr Val Asp Pro Val Gln 875 880 885	1296
TTC AAT CCT GTA CAG AAC CTG ACC GGT AGT GCA GTC GGC CAG AAA GTA Phe Asn Pro Val Gln Asn Leu Thr Gly Ser Ala Val Gly Gln Lys Val 890 895 900	1344
ACG CTT AAG TGG GAT GCA CCT AAT Thr Leu Lys Trp Asp Ala Pro Asn 905 910	1368

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 456 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn Pro Gly Thr Thr Thr Leu 1 5 10 15
Ser Glu Ser Phe Glu Asn Gly Ile Pro Ala Ser Trp Lys Thr Ile Asp 20 25 30

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Ala Asp Gly Asp Gly Asn Asn Trp Thr Thr Thr Pro Pro Pro Gly Gly
 35 40 45
 Thr Ser Phe Ala Gly His Asn Ser Ala Ile Cys Ala Ser Ser Ala Ser
 50 55 60
 Tyr Ile Asn Phe Glu Gly Pro Gln Asn Pro Asp Asn Tyr Leu Val Thr
 65 70 75 80
 Pro Glu Leu Ser Leu Pro Asn Gly Gly Thr Leu Thr Phe Trp Val Cys
 85 90 95
 Ala Gln Asp Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr Ala Ser
 100 105 110
 Ser Thr Gly Asn Asp Ala Ser Asn Phe Ala Asn Ala Leu Leu Glu Glu
 115 120 125
 Val Leu Thr Ala Lys Thr Val Val Thr Ala Pro Glu Ala Ile Arg Gly
 130 135 140
 Thr Arg Val Gln Gly Thr Trp Tyr Gln Lys Thr Val Gln Leu Pro Ala
 145 150 155 160
 Gly Thr Lys Tyr Val Ala Phe Arg His Phe Gly Cys Thr Asp Phe Phe
 165 170 175
 Trp Ile Asn Leu Asp Asp Val Glu Ile Lys Ala Asn Gly Lys Arg Ala
 180 185 190
 Asp Phe Thr Glu Thr Phe Glu Ser Ser Thr His Gly Glu Ala Pro Ala
 195 200 205
 Glu Trp Thr Thr Ile Asp Ala Asp Gly Asp Gly Gln Gly Trp Leu Cys
 210 215 220
 Leu Ser Ser Gly Gln Leu Gly Trp Leu Thr Ala His Gly Gly Thr Asn
 225 230 235 240
 Val Val Ala Ser Phe Ser Trp Asn Gly Met Ala Leu Asn Pro Asp Asn
 245 250 255
 Tyr Leu Ile Ser Lys Asp Val Thr Gly Ala Thr Lys Val Lys Tyr Tyr
 260 265 270
 Tyr Ala Val Asn Asp Gly Phe Pro Gly Asp His Tyr Ala Val Met Ile
 275 280 285
 Ser Lys Thr Gly Thr Asn Ala Gly Asp Phe Thr Val Val Phe Glu Glu
 290 295 300
 Thr Pro Asn Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly Leu Ser Thr
 305 310 315 320
 Glu Ala Asp Gly Ala Lys Pro Gln Ser Val Trp Ile Glu Arg Thr Val
 325 330 335
 Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys
 340 345 350
 Ser Asp Leu Asn Tyr Ile Leu Leu Asp Asp Ile Gln Phe Thr Met Gly
 355 360 365

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Gly Ser Pro Thr Pro Thr Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly
 370 375 380

Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr Thr Phe Glu Glu Asp Gly
 385 390 395 400

Val Ala Thr Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala
 405 410 415

Gly Val Ser Pro Lys Glu Cys Val Asn Val Thr Val Asp Pro Val Gln
 420 425 430

Phe Asn Pro Val Gln Asn Leu Thr Gly Ser Ala Val Gly Gln Lys Val
 435 440 445

Thr Leu Lys Trp Asp Ala Pro Asn
 450 455

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGT ACC CCG AAT CCA AAT CCA AAT CCG AAT CCG GGA ACA ACA ACA CTT	48
Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn Pro Gly Thr Thr Thr Leu	
460 465 470	
TCC GAA TCA TTC GAA AAT GGT ATT CCT GCC TCA TGG AAG ACG ATC GAT	96
Ser Glu Ser Phe Glu Asn Gly Ile Pro Ala Ser Trp Lys Thr Ile Asp	
475 480 485	
GCA GAC GGT GAC GGC AAC AAT TGG ACG ACG ACC CCT CCT CCC GGA GGC	144
Ala Asp Gly Asp Gly Asn Asn Trp Thr Thr Thr Pro Pro Pro Gly Gly	
490 495 500	
ACC TCT TTT GCA GGT CAC AAC AGT GCG ATC TGT GTC TCT TCG GCT TCT	192
Thr Ser Phe Ala Gly His Asn Ser Ala Ile Cys Val Ser Ser Ala Ser	
505 510 515 520	
TAT ATC AAC TTT GAA GGC CCT CAG AAC CCT GAT AAC TAT CTG GTT ACA	240
Tyr Ile Asn Phe Glu Gly Pro Gln Asn Pro Asp Asn Tyr Leu Val Thr	
525 530 535	
CCG GAG CTA TCT CTT CCT GGC GGA GGA ACG CTT ACT TTC TGG GTA TGT	288
Pro Glu Leu Ser Leu Pro Gly Gly Gly Thr Leu Thr Phe Trp Val Cys	
540 545 550	
GCA CAA GAT GCC AAT TAT GCA TCA GAG CAC TAT GCC GTG TAT GCA TCT	336
Ala Gln Asp Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr Ala Ser	
555 560 565	

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TCT ACG GGT AAC GAC GCT TCC AAC TTC GCC AAC GCT TTG TTG GAA GAA Ser Thr Gly Asn Asp Ala Ser Asn Phe Ala Asn Ala Leu Leu Glu Glu 570 575 580	384
GTG CTG ACG GCC AAG ACA GTT GTT ACG GCA CCT GAA GCC ATT CGT GGC Val Leu Thr Ala Lys Thr Val Val Thr Ala Pro Glu Ala Ile Arg Gly 585 590 595 600	432
ACT CGT GTT CAG GGC ACC TGG TAT CAA AAG ACG GTA CAG TTG CCT GCG Thr Arg Val Gln Gly Thr Trp Tyr Gln Lys Thr Val Gln Leu Pro Ala 605 610 615	480
GGT ACT AAG TAT GTT GCC TTC CGT CAC TTC GGC TGT ACG GAC TTC TTC Gly Thr Lys Tyr Val Ala Phe Arg His Phe Gly Cys Thr Asp Phe Phe 620 625 630	528
TGG ATC AAC CTT GAT GAA GTT GAG ATC AAG GCC AAC GGC AAG CGC GCA Trp Ile Asn Leu Asp Glu Val Glu Ile Lys Ala Asn Gly Lys Arg Ala 635 640 645	576
GAC TTC ACG GAA ACG TTC GAG TCT TCT ACT CAT GGA GAG GCA CCG GCG Asp Phe Thr Glu Thr Phe Glu Ser Ser Thr His Gly Glu Ala Pro Ala 650 655 660	624
GAA TGG ACT ACT ATC GAT GCC GAT GGC GAT GGT CAG GGT TGG CTC TGT Glu Trp Thr Thr Ile Asp Ala Asp Gly Asp Gln Gly Trp Leu Cys 665 670 675 680	672
CTG TCT TCC GGA CAA TTG GAC TGG CTG ACA GCT CAT GGC GGC ACC AAC Leu Ser Ser Gly Gln Leu Asp Trp Leu Thr Ala His Gly Gly Thr Asn 685 690 695	720
GTA GTA GCC TCT TTC TCA TGG AAT GGA ATG GCT TTG AAT CCT GAT AAC Val Val Ala Ser Phe Ser Trp Asn Gly Met Ala Leu Asn Pro Asp Asn 700 705 710	768
TAT CTC ATC TCA AAG GAT GTT ACA GGC GCA ACT AAG GTA AAG TAC TAC Tyr Leu Ile Ser Lys Asp Val Thr Gly Ala Thr Lys Val Lys Tyr Tyr 715 720 725	816
TAT GCA GTC AAC GAC GGT TTT CCC GGG GAT CAC TAT GCG GTG ATG ATC Tyr Ala Val Asn Asp Gly Phe Pro Gly Asp His Tyr Ala Val Met Ile 730 735 740	864
TCC AAG ACG GGC ACG AAC GCC GGA GAC TTC ACG GTT GTT TTC GAA GAA Ser Lys Thr Gly Thr Asn Ala Gly Asp Phe Thr Val Val Phe Glu Glu 745 750 755 760	912
ACG CCT AAC GGA ATA AAT AAG GGC GGA GCA AGA TTC GGT CTT TCC ACG Thr Pro Asn Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly Leu Ser Thr 765 770 775	960
GAA GCC GAT GGC GCC AAA CCT CAA AGT GTA TGG ATC GAG CGT ACG GTA Glu Ala Asp Gly Ala Lys Pro Gln Ser Val Trp Ile Glu Arg Thr Val 780 785 790	1008
GAT TTG CCT GCG GGC ACG AAG TAT GTT GCT TTC CGT CAC TAC AAT TGC Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys 795 800 805	1056
TCG GAT TTG AAC TAC ATT CTT TTG GAT GAT ATT CAG TTC ACC ATG GGT Ser Asp Leu Asn Tyr Ile Leu Leu Asp Asp Ile Gln Phe Thr Met Gly 810 815 820	1104

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GGC AGC CCC ACC CCG ACC GAT TAT ACC TAC ACG GTG TAT CGT GAC GGT	1152
Gly Ser Pro Thr Pro Thr Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly	
825 830 835 840	
ACG AAG ATC AAG GAA GGT CTG ACC GAA ACG ACC TTC GAA GAA GAT GGT	1200
Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr Thr Phe Glu Glu Asp Gly	
845 850 855	
GTA GCT ACG GGC AAT CAT GAG TAT TGC GTG GAA GTG AAG TAC ACA GCC	1248
Val Ala Thr Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala	
860 865 870	
GGC GTA TCT CCG AAG GTG TGT GTA AAC GTA ACT ATT AAT CCG ACT CAG	1296
Gly Val Ser Pro Lys Val Cys Val Asn Val Thr Ile Asn Pro Thr Gln	
875 880 885	
TTC AAT CCT GTA CAG AAC CTG A	1318
Phe Asn Pro Val Gln Asn Leu	
890 895	

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn Pro Gly Thr Thr Thr Leu	
1 5 10 15	
Ser Glu Ser Phe Glu Asn Gly Ile Pro Ala Ser Trp Lys Thr Ile Asp	
20 25 30	
Ala Asp Gly Asp Gly Asn Asn Trp Thr Thr Thr Pro Pro Gly Gly	
35 40 45	
Thr Ser Phe Ala Gly His Asn Ser Ala Ile Cys Val Ser Ser Ala Ser	
50 55 60	
Tyr Ile Asn Phe Glu Gly Pro Gln Asn Pro Asp Asn Tyr Leu Val Thr	
65 70 75 80	
Pro Glu Leu Ser Leu Pro Gly Gly Gly Thr Leu Thr Phe Trp Val Cys	
85 90 95	
Ala Gln Asp Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr Ala Ser	
100 105 110	
Ser Thr Gly Asn Asp Ala Ser Asn Phe Ala Asn Ala Leu Leu Glu Glu	
115 120 125	
Val Leu Thr Ala Lys Thr Val Val Thr Ala Pro Glu Ala Ile Arg Gly	
130 135 140	
Thr Arg Val Gln Gly Thr Trp Tyr Gln Lys Thr Val Gln Leu Pro Ala	
145 150 155 160	

115

Gly Thr Lys Tyr Val Ala Phe Arg His Phe Gly Cys Thr Asp Phe Phe
 165 170 175
 Trp Ile Asn Leu Asp Glu Val Glu Ile Lys Ala Asn Gly Lys Arg Ala
 180 185 190
 Asp Phe Thr Glu Thr Phe Glu Ser Ser Thr His Gly Glu Ala Pro Ala
 195 200 205
 Glu Trp Thr Thr Ile Asp Ala Asp Gly Asp Gly Gln Gly Trp Leu Cys
 210 215 220
 Leu Ser Ser Gly Gln Leu Asp Trp Leu Thr Ala His Gly Gly Thr Asn
 225 230 235 240
 Val Val Ala Ser Phe Ser Trp Asn Gly Met Ala Leu Asn Pro Asp Asn
 245 250 255
 Tyr Leu Ile Ser Lys Asp Val Thr Gly Ala Thr Lys Val Lys Tyr Tyr
 260 265 270
 Tyr Ala Val Asn Asp Gly Phe Pro Gly Asp His Tyr Ala Val Met Ile
 275 280 285
 Ser Lys Thr Gly Thr Asn Ala Gly Asp Phe Thr Val Val Phe Glu Glu
 290 295 300
 Thr Pro Asn Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly Leu Ser Thr
 305 310 315 320
 Glu Ala Asp Gly Ala Lys Pro Gln Ser Val Trp Ile Glu Arg Thr Val
 325 330 335
 Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys
 340 345 350
 Ser Asp Leu Asn Tyr Ile Leu Leu Asp Asp Ile Gln Phe Thr Met Gly
 355 360 365
 Gly Ser Pro Thr Pro Thr Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly
 370 375 380
 Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr Thr Phe Glu Glu Asp Gly
 385 390 395 400
 Val Ala Thr Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala
 405 410 415
 Gly Val Ser Pro Lys Val Cys Val Asn Val Thr Ile Asn Pro Thr Gln
 420 425 430
 Phe Asn Pro Val Gln Asn Leu
 435

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

116

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCAAACCAA AAAGATTC

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(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTCTTCCAAC GACTACAC

18

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 696..1787
- (D) OTHER INFORMATION: /product= "hagD protease"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1790..5866
- (D) OTHER INFORMATION: /product= "hagD hemagglutinin"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGATCCTACG CCCGATACCC ATACTCGAAG CCTTTGCTCA GTACCATCCT GCAGAAGTTC	60
ACTCTTTTCG ATATAGTGAC CCTCTTTTCT CTCAGCATAA TGGTACCTAT CATATCAGTA	120
AGGGGCATAT TGTCTTTTCG AACAAATGTAC AGCCCGAGAA CTCTTTACTT CCACATCACA	180
CCCCCGACTC CTTAGTCAAG GATCTTTTTT CCCCTTCCC CTCCGCTCTC TTCCTCATGC	240
TGGACTGACT TAACCTTGGT CTGCTCTACT TTTGGTTGT AAATACATGC AATACAATAA	300
CTTTAAGTGT TGTTAGACAA CACTTTTACA AGACTCTGAC TTTTAATGAG GTGGAGCATG	360
AACCTTTTCC TCTTTCATCT TCTATTGAG ATTATAGTCA ATATTTTAGT AAAAGGCTAA	420
TTGACAGCCT TTTATAAGGG TTAATCCCTT GTCGCTTATA TTGAAAACAT GTTCTTTATA	480
ATCCGATACT CTTCTTAAAT CGAATTTTTT CTCTAAATTG CGCCGCAACA AAACCTCCTG	540

AGAAAAGTAC	CAATAGAAAT	AGAAGGTAGC	ATTTTGCCTT	TAAATTCCTT	TTCTTTTCTT		600										
GGATTGTTCT	TGAAATGAAT	CTTATTTGTG	GATCTTTTTT	GTTTTTTTAA	CCCGGCCGTG		660										
GTTCTCTGAA	TCACGACCAT	AAATTGTTTT	AAAGT	ATG	AGG	AAA	TTA	TTA	TTG		713						
				Met	Arg	Lys	Leu	Leu	Leu								
				440						445							
CTG	ATC	GCG	GCG	TCC	CTT	TTG	GGA	GTT	GGT	CTT	TAC	GCC	CAA	AGC	GCC		761
Leu	Ile	Ala	Ala	Ser	Leu	Leu	Gly	Val	Gly	Leu	Tyr	Ala	Gln	Ser	Ala		
				450					455						460		
AAG	ATT	AAG	CTT	GAT	GCT	CCG	ACT	ACT	CGA	ACG	ACA	TGT	ACG	AAC	AAT		809
Lys	Ile	Lys	Leu	Asp	Ala	Pro	Thr	Thr	Arg	Thr	Thr	Cys	Thr	Asn	Asn		
			465					470						475			
AGC	TTC	AAG	CAG	TTC	GAT	GCA	AGC	TTT	TCG	TTC	AAT	GAA	GTC	GAG	CTG		857
Ser	Phe	Lys	Gln	Phe	Asp	Ala	Ser	Phe	Ser	Phe	Asn	Glu	Val	Glu	Leu		
		480					485					490					
ACA	AAG	GTG	GAG	ACC	AAA	GGT	GGT	ACT	TTC	GCC	TCA	GTG	TCA	ATT	CCG		905
Thr	Lys	Val	Glu	Thr	Lys	Gly	Gly	Thr	Phe	Ala	Ser	Val	Ser	Ile	Pro		
	495					500					505						
GGT	GCA	TTC	CCG	ACC	GGT	GAG	GTT	GGT	TCT	CCC	GAA	GTG	CCA	GCA	GTT		953
Gly	Ala	Phe	Pro	Thr	Gly	Glu	Val	Gly	Ser	Pro	Glu	Val	Pro	Ala	Val		
510					515					520					525		
AGG	AAG	TTG	ATT	GCT	GTG	CCT	GTC	GGA	GCC	ACA	CCT	GTT	GTT	CGC	GTG		1001
Arg	Lys	Leu	Ile	Ala	Val	Pro	Val	Gly	Ala	Thr	Pro	Val	Val	Arg	Val		
				530					535					540			
AAA	AGT	TTT	ACC	GAG	CAA	GTT	TAC	TCT	CTG	AAC	CAA	TAC	GGT	TCC	GAA		1049
Lys	Ser	Phe	Thr	Glu	Gln	Val	Tyr	Ser	Leu	Asn	Gln	Tyr	Gly	Ser	Glu		
			545					550					555				
AAA	CTC	ATG	CCA	CAT	CAA	CCC	TCT	ATG	AGC	AAG	AGT	GAT	GAT	CCC	GAA		1097
Lys	Leu	Met	Pro	His	Gln	Pro	Ser	Met	Ser	Lys	Ser	Asp	Asp	Pro	Glu		
		560					565					570					
AAG	GTT	CCC	TTC	GTT	TAC	AAT	GCT	GCT	GCT	TAT	GCA	CGC	AAA	GGT	TTT		1145
Lys	Val	Pro	Phe	Val	Tyr	Asn	Ala	Ala	Ala	Tyr	Ala	Arg	Lys	Gly	Phe		
	575					580					585						
GTC	GGA	CAA	GAA	CTG	ACC	CAA	GTA	GAA	ATG	TTG	GGG	ACA	ATG	CGT	GGT		1193
Val	Gly	Gln	Glu	Leu	Thr	Gln	Val	Glu	Met	Leu	Gly	Thr	Met	Arg	Gly		
590					595					600					605		
GTT	CGC	ATT	GCA	GCT	CTT	ACC	ATT	AAT	CCT	GTT	CAG	TAT	GAT	GTG	GTT		1241
Val	Arg	Ile	Ala	Ala	Leu	Thr	Ile	Asn	Pro	Val	Gln	Tyr	Asp	Val	Val		
			610						615					620			
GCA	AAC	CAA	TTG	AAG	GTT	AGA	AAC	AAC	ATC	GAA	ATT	GAA	GTA	AGC	TTT		1289
Ala	Asn	Gln															

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TAT ACA GAT CAT GGC GAC TTG TAT AAT ACG CCG GTT CGT ATG CTT GTT Tyr Thr Asp His Gly Asp Leu Tyr Asn Thr Pro Val Arg Met Leu Val 670 675 680 685	1433
GTT GCA GGT GCA AAA TTC AAA GAA GCT CTC AAG CCT TGG CTC ACT TGG Val Ala Gly Ala Lys Phe Lys Glu Ala Leu Lys Pro Trp Leu Thr Trp 690 695 700	1481
AAG GCT CAA AAG GGC TTC TAT CTG GAT GTG CAT TAC ACA GAC GAA GCT Lys Ala Gln Lys Gly Phe Tyr Leu Asp Val His Tyr Thr Asp Glu Ala 705 710 715	1529
GAA GTA GGA ACG ACA AAC GCC TCT ATC AAG GCA TTT ATT CAC AAG AAA Glu Val Gly Thr Thr Asn Ala Ser Ile Lys Ala Phe Ile His Lys Lys 720 725 730	1577
TAC AAT GAT GGA TTG GCA GCT AGT GCT GCT CCG GTC TTC TTG GCT TTG Tyr Asn Asp Gly Leu Ala Ala Ser Ala Ala Pro Val Phe Leu Ala Leu 735 740 745	1625
GTT GGT GAC ACT GAC GTT ATT AGC GGA GAA AAA GGA AAG AAA ACA AAA Val Gly Asp Thr Asp Val Ile Ser Gly Glu Lys Gly Lys Lys Thr Lys 750 755 760 765	1673
AAA GTT ACC GAC TTG TAT TAC AGT GCA GTC GAT GGC GAC TAT TTC CCT Lys Val Thr Asp Leu Tyr Tyr Ser Ala Val Asp Gly Asp Tyr Phe Pro 770 775 780	1721
GAA ATG TAT ACT TTC CGT ATG TCT GCT TCT TCC CCA GAA GAA CTG ACG Glu Met Tyr Thr Phe Arg Met Ser Ala Ser Ser Pro Glu Glu Leu Thr 785 790 795	1769
AAC ATC ATT GAT AAG TAT TG ATG TAT GAA AAG GCT ACC ATG CCG GAT Asn Ile Ile Asp Lys Tyr Met Tyr Glu Lys Ala Thr Met Pro Asp 800 1 5	1816
AAG AGC TAT TTG GAA AAG GCC CTC TTG ATT GCC GGT GCT GAC TCC TAC Lys Ser Tyr Leu Glu Lys Ala Leu Leu Ile Ala Gly Ala Asp Ser Tyr 10 15 20 25	1864
TGG AAT CCT AAG ATA GGC CAG CAA ACC ATC AAA TAT GCT GTA CAG TAT Trp Asn Pro Lys Ile Gly Gln Gln Thr Ile Lys Tyr Ala Val Gln Tyr 30 35 40	1912
TAC TAC AAT CAA GAT CAT GGC TAT ACA GAT GTG TAC AGT TAC CCT AAA Tyr Tyr Asn Gln Asp His Gly Tyr Thr Asp Val Tyr Ser Tyr Pro Lys 45 50 55	1960
GCT CCT TAT ACA GGC TGC TAT AGT CAC TTG AAT ACC GGT GTC GGC TTT Ala Pro Tyr Thr Gly Cys Tyr Ser His Leu Asn Thr Gly Val Gly Phe 60 65 70	2008
GCC AAC TAT ACA GCG CAT GGA TCT GAG ACA TCA TGG GCA GAT CCG TCG Ala Asn Tyr Thr Ala His Gly Ser Glu Thr Ser Trp Ala Asp Pro Ser 75 80 85	2056
CTG ACC GCC ACT CAA GTG AAA GCA CTC ACA AAT AAG GAC AAA TAC TTC Leu Thr Ala Thr Gln Val Lys Ala Leu Thr Asn Lys Asp Lys Tyr Phe 90 95 100 105	2104
TTA GCT ATT GGG AAC TGC TGT GTT ACA GCT CAA TTC GAT TAT CCA CAG Leu Ala Ile Gly Asn Cys Cys Val Thr Ala Gln Phe Asp Tyr Pro Gln 110 115 120	2152

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CCT TGC TTT GGA GAG GTA ATG ACT CGT GTC AAG GAG AAA GGT GCT TAT	2200
Pro Cys Phe Gly Glu Val Met Thr Arg Val Lys Glu Lys Gly Ala Tyr	
125 130 135	
GCC TAT ATC GGT TCA TCT CCG AAT TCT TAT TGG GGC GAG GAC TAC TAT	2248
Ala Tyr Ile Gly Ser Ser Pro Asn Ser Tyr Trp Gly Glu Asp Tyr Tyr	
140 145 150	
TGG AGT GTC GGT GCT AAT GCC GTA TTT GGT GTT CAG CCT ACT TTT GAA	2296
Trp Ser Val Gly Ala Asn Ala Val Phe Gly Val Gln Pro Thr Phe Glu	
155 160 165	
GGT ACG TCT ATG GGT TCT TAT GAT GCT ACA TTC TTG GAA GAT TCG TAC	2344
Gly Thr Ser Met Gly Ser Tyr Asp Ala Thr Phe Leu Glu Asp Ser Tyr	
170 175 180 185	
AAC ACA GTG AAT TCT ATT ATG TGG GCA GGT AAT CTT GCC GCT ACT CAT	2392
Asn Thr Val Asn Ser Ile Met Trp Ala Gly Asn Leu Ala Ala Thr His	
190 195 200	
GCT GGA AAT ATC GGC AAT ATT ACC CAT ATC GGT GCT CAT TAC TAT TGG	2440
Ala Gly Asn Ile Gly Asn Ile Thr His Ile Gly Ala His Tyr Tyr Trp	
205 210 215	
GAA GCT TAT CAT GTC CTT GGC GAT GGT TCG GTT ATG CCT TAT CGT GCA	2488
Glu Ala Tyr His Val Leu Gly Asp Gly Ser Val Met Pro Tyr Arg Ala	
220 225 230	
ATG CCT AAG ACC AAT ACT TAT ACG CTT CCT GCT TCT CTG CCT CAG AAT	2536
Met Pro Lys Thr Asn Thr Tyr Thr Leu Pro Ala Ser Leu Pro Gln Asn	
235 240 245	
CAG GCT TCT TAT AGC ATT CAG GCT TCT GCC GGT TCT TAC GTA GCT ATT	2584
Gln Ala Ser Tyr Ser Ile Gln Ala Ser Ala Gly Ser Tyr Val Ala Ile	
250 255 260 265	
TCT AAA GAT GGA GTT TTG TAT GGA ACA GGT GTT GCT AAT GCC AGC GGT	2632
Ser Lys Asp Gly Val Leu Tyr Gly Thr Gly Val Ala Asn Ala Ser Gly	
270 275 280	
GTT GCG ACT GTG AAT ATG ACT AAG CAG ATT ACG GAA AAT GGT AAT TAT	2680
Val Ala Thr Val Asn Met Thr Lys Gln Ile Thr Glu Asn Gly Asn Tyr	
285 290 295	
GAT GTA GTT ATC ACT CGC TCT AAT TAT CTT CCT GTG ATC AAG CAA ATT	2728
Asp Val Val Ile Thr Arg Ser Asn Tyr Leu Pro Val Ile Lys Gln Ile	
300 305 310	
CAG GCA GGA GAG CCT AGC CCC TAC CAG CCT GTT TCC AAC TTG ACT GCT	2776
Gln Ala Gly Glu Pro Ser Pro Tyr Gln Pro Val Ser Asn Leu Thr Ala	
315 320 325	
ACA ACG CAG GGT CAG AAA GTA ACG CTC AAG TGG GAT GCC CCG AGC GCA	2824
Thr Thr Gln Gly Gln Lys Val Thr Leu Lys Trp Asp Ala Pro Ser Ala	
330 335 340 345	
AAG AAG GCA GAA GCT TCC CGT GAA GTA AAA CGG ATC GGA GAC GGT CTT	2872
Lys Lys Ala Glu Ala Ser Arg Glu Val Lys Arg Ile Gly Asp Gly Leu	
350 355 360	
TTC GTT ACG ATC GAA CCT GCA AAC GAT GTA CGT GCC AAC GAA GCC AAG	2920
Phe Val Thr Ile Glu Pro Ala Asn Asp Val Arg Ala Asn Glu Ala Lys	
365 370 375	

120

GTT GTG CTC GCA GCA GAC AAC GTA TGG GGA GAC AAT ACG GGT TAC CAG Val Val Leu Ala Ala Asp Asn Val Trp Gly Asp Asn Thr Gly Tyr Gln 380 385 390	2968
TTC TTG TTG GAT GCC GAT CAC AAT ACA TTC GGA AGT GTC ATT CCG GCA Phe Leu Leu Asp Ala Asp His Asn Thr Phe Gly Ser Val Ile Pro Ala 395 400 405	3016
ACC GGT CCT CTC TTT ACC GGA ACA GCT TCT TCC AAT CTT TAC AGT GCG Thr Gly Pro Leu Phe Thr Gly Thr Ala Ser Ser Asn Leu Tyr Ser Ala 410 415 420 425	3064
AAC TTC GAG TAT TTG ATC CCG GCC AAT GCC GAT CCT GTT GTT ACT ACA Asn Phe Glu Tyr Leu Ile Pro Ala Asn Ala Asp Pro Val Val Thr Thr 430 435 440	3112
CAG AAT ATT ATC GTT ACA GGA CAG GGT GAA GTT GTA ATC CCC GGT GGT Gln Asn Ile Val Thr Gly Gln Gly Glu Val Val Ile Pro Gly Gly 445 450 455	3160
GTT TAC GAC TAT TGC ATT ACG AAC CCG GAA CCT GCA TCC GGA AAG ATG Val Tyr Asp Tyr Cys Ile Thr Asn Pro Glu Pro Ala Ser Gly Lys Met 460 465 470	3208
TGG ATC GCA GGA GAT GGA GAC AAC CAG CCT GCA CGT TAT GAC GAT TTC Trp Ile Ala Gly Asp Gly Asp Asn Gln Pro Ala Arg Tyr Asp Asp Phe 475 480 485	3256
ACA TTC GAA GCA GGC AAG AAG TAC ACC TTC ACG ATG CGT CGC GCC GGA Thr Phe Glu Ala Gly Lys Lys Tyr Thr Phe Thr Met Arg Arg Ala Gly 490 495 500 505	3304
ATG GGA GAT GGA ACT GAT ATG GAA GTC GAA GAC GAT TCA CCT GCA AGC Met Gly Asp Gly Thr Asp Met Glu Val Glu Asp Asp Ser Pro Ala Ser 510 515 520	3352
TAT ACC TAT ACA GTC TAT CGT GAC GGC ACG AAG ATC AAG GAA GGT CTG Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Thr Lys Ile Lys Glu Gly Leu 525 530 535	3400
ACG GCT ACG ACA TTC GAA GAA GAC GGT GTA GCT GCA GGC AAT CAT GAG Thr Ala Thr Thr Phe Glu Glu Asp Gly Val Ala Ala Gly Asn His Glu 540 545 550	3448
TAT TGC GTG GAA GTT AAG TAC ACA GCC GGC GTA TCT CCG AAG GTA TGT Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Val Cys 555 560 565	3496
AAA GAC GTT ACG GTA GAA GGA TCC AAT GAA TTT GCT CCT GTA CAG AAC Lys Asp Val Thr Val Glu Gly Ser Asn Glu Phe Ala Pro Val Gln Asn 570 575 580 585	3544
CTG ACC GGT AGT GCA GTC GGC CAG AAA GTA ACG CTT AAG TGG GAT GCA Leu Thr Gly Ser Ala Val Gly Gln Lys Val Thr Leu Lys Trp Asp Ala 590 595 600	3592
CCT AAT GGT ACC CCA AAT CCG AAT CCG AAT CCG AAT CCG GGA ACA ACA Pro Asn Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn Pro Gly Thr Thr 605 610 615	3640
ACA CTT TCC GAA TCA TTC GAA AAT GGT ATT CCT GCC TCA TGG AAG ACG Thr Leu Ser Glu Ser Phe Glu Asn Gly Ile Pro Ala Ser Trp Lys Thr 620 625 630	3688

121

ATC GAT GCA GAC GGT GAC GGG CAT GGC TGG AAA CCT GGA AAT GCT CCC Ile Asp Ala Asp Gly Asp Gly His Gly Trp Lys Pro Gly Asn Ala Pro 635 640 645	3736
GGA ATC GCT GGC TAC AAT AGC AAT GGT TGT GTA TAT TCA GAG TCA TTC Gly Ile Ala Gly Tyr Asn Ser Asn Gly Cys Val Tyr Ser Glu Ser Phe 650 655 660 665	3784
GGT CTT GGT GGT ATA GGA GTT CTT ACC CCT GAC AAC TAT CTG ATA ACA Gly Leu Gly Gly Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Ile Thr 670 675 680	3832
CCG GCA TTG GAT TTG GCT AAC GGA GGT AAG TTG ACT TTC TGG GTA TGC Pro Ala Leu Asp Leu Ala Asn Gly Gly Lys Leu Thr Phe Trp Val Cys 685 690 695	3880
GCA CAG GAT GCT AAT TAT GCA TCC GAG CAC TAT GCG GTG TAT GCA TCT Ala Gln Asp Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr Ala Ser 700 705 710	3928
TCG ACC GGT AAC GAT GCA TCC AAC TTC ACG AAT GCT TTG TTG GAA GAG Ser Thr Gly Asn Asp Ala Ser Asn Phe Thr Asn Ala Leu Leu Glu Glu 715 720 725	3976
ACG ATT ACG GCA AAA GGT GTT CGC TCG CCG GAA GCT ATT CGT GGT CGT Thr Ile Thr Ala Lys Gly Val Arg Ser Pro Glu Ala Ile Arg Gly Arg 730 735 740 745	4024
ATA CAG GGT ACT TGG CGC CAG AAG ACG GTA GAC CTT CCC GCA GGT ACG Ile Gln Gly Thr Trp Arg Gln Lys Thr Val Asp Leu Pro Ala Gly Thr 750 755 760	4072
AAA TAT GTT GCT TTC CGT CAC TTC CAA AGC ACG GAT ATG TTC TAC ATC Lys Tyr Val Ala Phe Arg His Phe Gln Ser Thr Asp Met Phe Tyr Ile 765 770 775	4120
GAC CTT GAT GAG GTT GAG ATC AAG GCC AAT GGC AAG CGC GCA GAC TTC Asp Leu Asp Glu Val Glu Ile Lys Ala Asn Gly Lys Arg Ala Asp Phe 780 785 790	4168
ACG GAA ACG TTC GAG TCT TCT ACT CAT GGA GAG GCA CCA GCG GAA TGG Thr Glu Thr Phe Glu Ser Ser Thr His Gly Glu Ala Pro Ala Glu Trp 795 800 805	4216
ACT ACT ATC GAT GCC GAT GGC GAT GGT CAG GAT TGG CTC TGT CTG TCT Thr Thr Ile Asp Ala Asp Gly Asp Gly Gln Asp Trp Leu Cys Leu Ser 810 815 820 825	4264
TCC GGA CAA TTG GAC TGG CTG ACA GCT CAT GGC GGC ACC AAC GTA GTA Ser Gly Gln Leu Asp Trp Leu Thr Ala His Gly Gly Thr Asn Val Val 830 835 840	4312
GCC TCT TTC TCA TGG AAT GGA ATG GCT TTG AAT CCT GAT AAC TAT CTC Ala Ser Phe Ser Trp Asn Gly Met Ala Leu Asn Pro Asp Asn Tyr Leu 845 850 855	4360
ATC TCA AAG GAT GTT ACA GGC GCA ACG AAG GTA AAG TAC TAC TAT GCA Ile Ser Lys Asp Val Thr Gly Ala Thr Lys Val Lys Tyr Tyr Tyr Ala 860 865 870	4408
GTC AAC GAC GGT TTT CCC GGG GAT CAC TAT GCG GTG ATG ATC TCC AAG Val Asn Asp Gly Phe Pro Gly Asp His Tyr Ala Val Met Ile Ser Lys 875 880 885	4456

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ACG GGC ACG AAC GCC GGA GAC TTC ACG GTT GTT TTC GAA GAA ACG CCT Thr Gly Thr Asn Ala Gly Asp Phe Thr Val Val Phe Glu Glu Thr Pro 890 895 900 905	4504
AAC GGA ATA AAT AAG GGC GGA GCA AGA TTC GGT CTT TCC ACG GAA GCC Asn Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly Leu Ser Thr Glu Ala 910 915 920	4552
AAT GGC GCC AAA CCT CAA AGT GTA TGG ATC GAG CGT ACG GTA GAT TTG Asn Gly Ala Lys Pro Gln Ser Val Trp Ile Glu Arg Thr Val Asp Leu 925 930 935	4600
CCT GCG GGC ACG AAG TAT GTT GCT TTC CGT CAC TAC AAT TGC TCG GAT Pro Ala Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys Ser Asp 940 945 950	4648
TTG GAC TAC ATT CTT TTG GAT GAT ATT CAG TTC ACC ATG GGT GGC AGC Leu Asp Tyr Ile Leu Leu Asp Asp Ile Gln Phe Thr Met Gly Gly Ser 955 960 965	4696
CCC ACC CCG ACC GAT TAT ACC TAC ACG GTA TAT CGT GAT GGT ACG AAG Pro Thr Pro Thr Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Thr Lys 970 975 980 985	4744
ATC AAG GAA GGT CTG ACC GAA ACG ACC TTC GAA GAA GAC GGC GTA GCT Ile Lys Glu Gly Leu Thr Glu Thr Thr Phe Glu Glu Asp Gly Val Ala 990 995 1000	4792
ACG GGC AAT CAT GAG TAT TGC GTG GAA GTG AAG TAC ACA GCC GGC GTA Thr Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly Val 1005 1010 1015	4840
TCT CCG AAG GTG TGT GTA AAC GTA ACT ATT AAT CCG ACT CAG TTC AAT Ser Pro Lys Val Cys Val Asn Val Thr Ile Asn Pro Thr Gln Phe Asn 1020 1025 1030	4888
CCT GTA AAG AAC CTG AAG GCA CAA CCG GAT GGC GGC GAC GTG GTT CTC Pro Val Lys Asn Leu Lys Ala Gln Pro Asp Gly Gly Asp Val Val Leu 1035 1040 1045	4936
AAG TGG GAA GCC CCG AGT GGC AAA CGA GGA GAA CTG CTT AAT GAA GAT Lys Trp Glu Ala Pro Ser Gly Lys Arg Gly Glu Leu Leu Asn Glu Asp 1050 1055 1060 1065	4984
TTT GAA GGA GAC GCT ATT CCC ACA GGG TGG ACA GCA TTG GAT GCC GAT Phe Glu Gly Asp Ala Ile Pro Thr Gly Trp Thr Ala Leu Asp Ala Asp 1070 1075 1080	5032
GGT GAC GGT AAT AAC TGG GAT ATC ACG CTC AAT GAA TTT ACG CGA GGA Gly Asp Gly Asn Asn Trp Asp Ile Thr Leu Asn Glu Phe Thr Arg Gly 1085 1090 1095	5080
GAG CGT CAT GTT CTT TCA CCT TTA CGC GCC AGC AAC GTA GCC ATA TCC Glu Arg His Val Leu Ser Pro Leu Arg Ala Ser Asn Val Ala Ile Ser 1100 1105 1110	5128
TAT TCT TCT TTA CTT CAG GGT CAA GAA TAT TTG CCT CTC ACG CCG AAC Tyr Ser Ser Leu Leu Gln Gly Gln Glu Tyr Leu Pro Leu Thr Pro Asn 1115 1120 1125	5176
AAC TTT CTG ATC ACT CCG AAG GTT GAA GGA GCA AAG AAG ATT ACT TAT Asn Phe Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Lys Ile Thr Tyr 1130 1135 1140 1145	5224

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AAG GTG GGT TCA CCG GGT CTT CCT CAA TGG AGT CAT GAT CAT TAT GCA Lys Val Gly Ser Pro Gly Leu Pro Gln Trp Ser His Asp His Tyr Ala 1150 1155 1160	5272
CTC TGT ATC TCC AAG AGC GGA ACG GCT GCA GCC GAC TTC GAA GTA ATC Leu Cys Ile Ser Lys Ser Gly Thr Ala Ala Ala Asp Phe Glu Val Ile 1165 1170 1175	5320
TTT GAA GAA ACG ATG ACC TAC ACT CAA GGA GGA GCC AAC TTG ACA AGA Phe Glu Glu Thr Met Thr Tyr Thr Gln Gly Gly Ala Asn Leu Thr Arg 1180 1185 1190	5368
GAA AAA GAC CTC CCT GCC GGC ACG AAA TAT GTC GCT TTC CGT CAT TAC Glu Lys Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Tyr 1195 1200 1205	5416
AAT TGC ACG GAT GTT CTG GGC ATA ATG ATT GAC GAT GTA GTG ATA ACA Asn Cys Thr Asp Val Leu Gly Ile Met Ile Asp Asp Val Val Ile Thr 1210 1215 1220 1225	5464
GGT GAA GGC GAA GGT CCC AGT TAC ACC TAC ACG GTG TAT CGT GAC GGC Gly Glu Gly Glu Gly Pro Ser Tyr Thr Tyr Thr Val Tyr Arg Asp Gly 1230 1235 1240	5512
ACG AAG ATC CAG GAA GGT CTG ACC GAA ACG ACC TAC CGC GAT GCA GGA Thr Lys Ile Gln Glu Gly Leu Thr Glu Thr Thr Tyr Arg Asp Ala Gly 1245 1250 1255	5560
ATG AGT GCA CAA TCT CAT GAG TAT TGC GTA GAG GTT AAG TAC GCA GCC Met Ser Ala Gln Ser His Glu Tyr Cys Val Glu Val Lys Tyr Ala Ala 1260 1265 1270	5608
GGC GTA TCT CCG AAG GTT TGT GTG GAT TAT ATT CCT GAT GGA GTG GCA Gly Val Ser Pro Lys Val Cys Val Asp Tyr Ile Pro Asp Gly Val Ala 1275 1280 1285	5656
GAC GTA ACT GCT CAG AAG CCT TAC ACG CTG ACG GTT GTA GGA AAG ACT Asp Val Thr Ala Gln Lys Pro Tyr Thr Leu Thr Val Val Gly Lys Thr 1290 1295 1300 1305	5704
ATC ACG GTA ACT TGC CAA GGC GAA GCT ATG ATC TAC GAC ATG AAC GGT Ile Thr Val Thr Cys Gln Gly Glu Ala Met Ile Tyr Asp Met Asn Gly 1310 1315 1320	5752
CGT CGT CTG GCA GCG GGT CGC AAC ACG GTT GTT TAC ACG GCT CAG GGC Arg Arg Leu Ala Ala Gly Arg Asn Thr Val Val Tyr Thr Ala Gln Gly 1325 1330 1335	5800
GGC TAC TAT GCA GTC ATG GTT GTC GTT GAC GGC AAG TCT TAC GTA GAG Gly Tyr Tyr Ala Val Met Val Val Val Asp Gly Lys Ser Tyr Val Glu 1340 1345 1350	5848
AAA CTC GCT ATC AAG TAA TTCTGTCTTG GACTCGGAGA CTTTGTGCAG Lys Leu Ala Ile Lys 1355	5896
ACACTTTTAA TATAGGTCTG TAATTGTCTC AGAGTATGAA TCGGTCGCCC GACTTCCTTA	5956
AAAGGAGGTC GGGCGACTTC GTTTTTATTA TTGCTGTCTG GTAAACTTGT CAAGAGGAGA	6016
CCTTTGAAAA ATGGGGCGGT CAATAATTTT CGGTCTATGG GTCAAATTGC AGGCTACTGT	6076
TTTAGGTGTA TGTTGGGCTA TCTTCCTATC TTAAAGAGAC CTTTGAAAAA TAAGGAGATG	6136

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GAGGGAAGAG GAGTTCTTGG CATAAAAGGA GCGAGTGAAA GGGGTGGCAG TAAGGAGTGA 6196
 AAGTAGTTGT AAATCCCCC TTTGAGGAGC TACTTGTACG AGCTC 6241

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 364 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Arg Lys Leu Leu Leu Ile Ala Ala Ser Leu Leu Gly Val Gly
 1 5 10 15
 Leu Tyr Ala Gln Ser Ala Lys Ile Lys Leu Asp Ala Pro Thr Thr Arg
 20 25 30
 Thr Thr Cys Thr Asn Asn Ser Phe Lys Gln Phe Asp Ala Ser Phe Ser
 35 40 45
 Phe Asn Glu Val Glu Leu Thr Lys Val Glu Thr Lys Gly Gly Thr Phe
 50 55 60
 Ala Ser Val Ser Ile Pro Gly Ala Phe Pro Thr Gly Glu Val Gly Ser
 65 70 75 80
 Pro Glu Val Pro Ala Val Arg Lys Leu Ile Ala Val Pro Val Gly Ala
 85 90 95
 Thr Pro Val Val Arg Val Lys Ser Phe Thr Glu Gln Val Tyr Ser Leu
 100 105 110
 Asn Gln Tyr Gly Ser Glu Lys Leu Met Pro His Gln Pro Ser Met Ser
 115 120 125
 Lys Ser Asp Asp Pro Glu Lys Val Pro Phe Val Tyr Asn Ala Ala Ala
 130 135 140
 Tyr Ala Arg Lys Gly Phe Val Gly Gln Glu Leu Thr Gln Val Glu Met
 145 150 155 160
 Leu Gly Thr Met Arg Gly Val Arg Ile Ala Ala Leu Thr Ile Asn Pro
 165 170 175
 Val Gln Tyr Asp Val Val Ala Asn Gln Leu Lys Val Arg Asn Asn Ile
 180 185 190
 Glu Ile Glu Val Ser Phe Gln Gly Ala Asp Glu Val Ala Thr Gln Arg
 195 200 205
 Leu Tyr Asp Ala Ser Phe Ser Pro Tyr Phe Glu Thr Ala Tyr Lys Gln
 210 215 220
 Leu Phe Asn Arg Asp Val Tyr Thr Asp His Gly Asp Leu Tyr Asn Thr
 225 230 235 240
 Pro Val Arg Met Leu Val Val Ala Gly Ala Lys Phe Lys Glu Ala Leu
 245 250 255

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Lys Pro Trp Leu Thr Trp Lys Ala Gln Lys Gly Phe Tyr Leu Asp Val
 260 265 270
 His Tyr Thr Asp Glu Ala Glu Val Gly Thr Thr Asn Ala Ser Ile Lys
 275 280 285
 Ala Phe Ile His Lys Lys Tyr Asn Asp Gly Leu Ala Ala Ser Ala Ala
 290 295 300
 Pro Val Phe Leu Ala Leu Val Gly Asp Thr Asp Val Ile Ser Gly Glu
 305 310 315 320
 Lys Gly Lys Lys Thr Lys Lys Val Thr Asp Leu Tyr Tyr Ser Ala Val
 325 330 335
 Asp Gly Asp Tyr Phe Pro Glu Met Tyr Thr Phe Arg Met Ser Ala Ser
 340 345 350
 Ser Pro Glu Glu Leu Thr Asn Ile Ile Asp Lys Tyr
 355 360

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1358 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Tyr Glu Lys Ala Thr Met Pro Asp Lys Ser Tyr Leu Glu Lys Ala
 1 5 10 15
 Leu Leu Ile Ala Gly Ala Asp Ser Tyr Trp Asn Pro Lys Ile Gly Gln
 20 25 30
 Gln Thr Ile Lys Tyr Ala Val Gln Tyr Tyr Tyr Asn Gln Asp His Gly
 35 40 45
 Tyr Thr Asp Val Tyr Ser Tyr Pro Lys Ala Pro Tyr Thr Gly Cys Tyr
 50 55 60
 Ser His Leu Asn Thr Gly Val Gly Phe Ala Asn Tyr Thr Ala His Gly
 65 70 75 80
 Ser Glu Thr Ser Trp Ala Asp Pro Ser Leu Thr Ala Thr Gln Val Lys
 85 90 95
 Ala Leu Thr Asn Lys Asp Lys Tyr Phe Leu Ala Ile Gly Asn Cys Cys
 100 105 110
 Val Thr Ala Gln Phe Asp Tyr Pro Gln Pro Cys Phe Gly Glu Val Met
 115 120 125
 Thr Arg Val Lys Glu Lys Gly Ala Tyr Ala Tyr Ile Gly Ser Ser Pro
 130 135 140
 Asn Ser Tyr Trp Gly Glu Asp Tyr Tyr Trp Ser Val Gly Ala Asn Ala
 145 150 155 160

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Val Phe Gly Val Gln Pro Thr Phe Glu Gly Thr Ser Met Gly Ser Tyr
 165 170 175
 Asp Ala Thr Phe Leu Glu Asp Ser Tyr Asn Thr Val Asn Ser Ile Met
 180 185 190
 Trp Ala Gly Asn Leu Ala Ala Thr His Ala Gly Asn Ile Gly Asn Ile
 195 200 205
 Thr His Ile Gly Ala His Tyr Tyr Trp Glu Ala Tyr His Val Leu Gly
 210 215 220
 Asp Gly Ser Val Met Pro Tyr Arg Ala Met Pro Lys Thr Asn Thr Tyr
 225 230 235 240
 Thr Leu Pro Ala Ser Leu Pro Gln Asn Gln Ala Ser Tyr Ser Ile Gln
 245 250 255
 Ala Ser Ala Gly Ser Tyr Val Ala Ile Ser Lys Asp Gly Val Leu Tyr
 260 265 270
 Gly Thr Gly Val Ala Asn Ala Ser Gly Val Ala Thr Val Asn Met Thr
 275 280 285
 Lys Gln Ile Thr Glu Asn Gly Asn Tyr Asp Val Val Ile Thr Arg Ser
 290 295 300
 Asn Tyr Leu Pro Val Ile Lys Gln Ile Gln Ala Gly Glu Pro Ser Pro
 305 310 315 320
 Tyr Gln Pro Val Ser Asn Leu Thr Ala Thr Thr Gln Gly Gln Lys Val
 325 330 335
 Thr Leu Lys Trp Asp Ala Pro Ser Ala Lys Lys Ala Glu Ala Ser Arg
 340 345 350
 Glu Val Lys Arg Ile Gly Asp Gly Leu Phe Val Thr Ile Glu Pro Ala
 355 360 365
 Asn Asp Val Arg Ala Asn Glu Ala Lys Val Val Leu Ala Ala Asp Asn
 370 375 380
 Val Trp Gly Asp Asn Thr Gly Tyr Gln Phe Leu Leu Asp Ala Asp His
 385 390 395 400
 Asn Thr Phe Gly Ser Val Ile Pro Ala Thr Gly Pro Leu Phe Thr Gly
 405 410 415
 Thr Ala Ser Ser Asn Leu Tyr Ser Ala Asn Phe Glu Tyr Leu Ile Pro
 420 425 430
 Ala Asn Ala Asp Pro Val Val Thr Thr Gln Asn Ile Ile Val Thr Gly
 435 440 445
 Gln Gly Glu Val Val Ile Pro Gly Gly Val Tyr Asp Tyr Cys Ile Thr
 450 455 460
 Asn Pro Glu Pro Ala Ser Gly Lys Met Trp Ile Ala Gly Asp Gly Asp
 465 470 475 480
 Asn Gln Pro Ala Arg Tyr Asp Asp Phe Thr Phe Glu Ala Gly Lys Lys
 485 490 495

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Tyr Thr Phe Thr Met Arg Arg Ala Gly Met Gly Asp Gly Thr Asp Met
 500 505 510
 Glu Val Glu Asp Asp Ser Pro Ala Ser Tyr Thr Tyr Thr Val Tyr Arg
 515 520 525
 Asp Gly Thr Lys Ile Lys Glu Gly Leu Thr Ala Thr Thr Phe Glu Glu
 530 535 540
 Asp Gly Val Ala Ala Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr
 545 550 555 560
 Thr Ala Gly Val Ser Pro Lys Val Cys Lys Asp Val Thr Val Glu Gly
 565 570 575
 Ser Asn Glu Phe Ala Pro Val Gln Asn Leu Thr Gly Ser Ala Val Gly
 580 585 590
 Gln Lys Val Thr Leu Lys Trp Asp Ala Pro Asn Gly Thr Pro Asn Pro
 595 600 605
 Asn Pro Asn Pro Asn Pro Gly Thr Thr Thr Leu Ser Glu Ser Phe Glu
 610 615 620
 Asn Gly Ile Pro Ala Ser Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly
 625 630 635 640
 His Gly Trp Lys Pro Gly Asn Ala Pro Gly Ile Ala Gly Tyr Asn Ser
 645 650 655
 Asn Gly Cys Val Tyr Ser Glu Ser Phe Gly Leu Gly Gly Ile Gly Val
 660 665 670
 Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro Ala Leu Asp Leu Ala Asn
 675 680 685
 Gly Gly Lys Leu Thr Phe Trp Val Cys Ala Gln Asp Ala Asn Tyr Ala
 690 695 700
 Ser Glu His Tyr Ala Val Tyr Ala Ser Ser Thr Gly Asn Asp Ala Ser
 705 710 715 720
 Asn Phe Thr Asn Ala Leu Leu Glu Glu Thr Ile Thr Ala Lys Gly Val
 725 730 735
 Arg Ser Pro Glu Ala Ile Arg Gly Arg Ile Gln Gly Thr Trp Arg Gln
 740 745 750
 Lys Thr Val Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His
 755 760 765
 Phe Gln Ser Thr Asp Met Phe Tyr Ile Asp Leu Asp Glu Val Glu Ile
 770 775 780
 Lys Ala Asn Gly Lys Arg Ala Asp Phe Thr Glu Thr Phe Glu Ser Ser
 785 790 795 800
 Thr His Gly Glu Ala Pro Ala Glu Trp Thr Thr Ile Asp Ala Asp Gly
 805 810 815
 Asp Gly Gln Asp Trp Leu Cys Leu Ser Ser Gly Gln Leu Asp Trp Leu
 820 825 830

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Thr Ala His Gly Gly Thr Asn Val Val Ala Ser Phe Ser Trp Asn Gly
 835 840 845
 Met Ala Leu Asn Pro Asp Asn Tyr Leu Ile Ser Lys Asp Val Thr Gly
 850 855 860
 Ala Thr Lys Val Lys Tyr Tyr Tyr Ala Val Asn Asp Gly Phe Pro Gly
 865 870 875 880
 Asp His Tyr Ala Val Met Ile Ser Lys Thr Gly Thr Asn Ala Gly Asp
 885 890 895
 Phe Thr Val Val Phe Glu Glu Thr Pro Asn Gly Ile Asn Lys Gly Gly
 900 905 910
 Ala Arg Phe Gly Leu Ser Thr Glu Ala Asn Gly Ala Lys Pro Gln Ser
 915 920 925
 Val Trp Ile Glu Arg Thr Val Asp Leu Pro Ala Gly Thr Lys Tyr Val
 930 935 940
 Ala Phe Arg His Tyr Asn Cys Ser Asp Leu Asp Tyr Ile Leu Leu Asp
 945 950 955 960
 Asp Ile Gln Phe Thr Met Gly Gly Ser Pro Thr Pro Thr Asp Tyr Thr
 965 970 975
 Tyr Thr Val Tyr Arg Asp Gly Thr Lys Ile Lys Glu Gly Leu Thr Glu
 980 985 990
 Thr Thr Phe Glu Glu Asp Gly Val Ala Thr Gly Asn His Glu Tyr Cys
 995 1000 1005
 Val Glu Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Val Cys Val Asn
 1010 1015 1020
 Val Thr Ile Asn Pro Thr Gln Phe Asn Pro Val Lys Asn Leu Lys Ala
 1025 1030 1035 1040
 Gln Pro Asp Gly Gly Asp Val Val Leu Lys Trp Glu Ala Pro Ser Gly
 1045 1050 1055
 Lys Arg Gly Glu Leu Leu Asn Glu Asp Phe Glu Gly Asp Ala Ile Pro
 1060 1065 1070
 Thr Gly Trp Thr Ala Leu Asp Ala Asp Gly Asp Gly Asn Asn Trp Asp
 1075 1080 1085
 Ile Thr Leu Asn Glu Phe Thr Arg Gly Glu Arg His Val Leu Ser Pro
 1090 1095 1100
 Leu Arg Ala Ser Asn Val Ala Ile Ser Tyr Ser Ser Leu Leu Gln Gly
 1105 1110 1115 1120
 Gln Glu Tyr Leu Pro Leu Thr Pro Asn Asn Phe Leu Ile Thr Pro Lys
 1125 1130 1135
 Val Glu Gly Ala Lys Lys Ile Thr Tyr Lys Val Gly Ser Pro Gly Leu
 1140 1145 1150
 Pro Gln Trp Ser His Asp His Tyr Ala Leu Cys Ile Ser Lys Ser Gly
 1155 1160 1165

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Thr Ala Ala Ala Asp Phe Glu Val Ile Phe Glu Glu Thr Met Thr Tyr
 1170 1175 1180
 Thr Gln Gly Gly Ala Asn Leu Thr Arg Glu Lys Asp Leu Pro Ala Gly
 1185 1190 1195 1200
 Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys Thr Asp Val Leu Gly
 1205 1210 1215
 Ile Met Ile Asp Asp Val Val Ile Thr Gly Glu Gly Glu Gly Pro Ser
 1220 1225 1230
 Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Thr Lys Ile Gln Glu Gly Leu
 1235 1240 1245
 Thr Glu Thr Thr Tyr Arg Asp Ala Gly Met Ser Ala Gln Ser His Glu
 1250 1255 1260
 Tyr Cys Val Glu Val Lys Tyr Ala Ala Gly Val Ser Pro Lys Val Cys
 1265 1270 1275 1280
 Val Asp Tyr Ile Pro Asp Gly Val Ala Asp Val Thr Ala Gln Lys Pro
 1285 1290 1295
 Tyr Thr Leu Thr Val Val Gly Lys Thr Ile Thr Val Thr Cys Gln Gly
 1300 1305 1310
 Glu Ala Met Ile Tyr Asp Met Asn Gly Arg Arg Leu Ala Ala Gly Arg
 1315 1320 1325
 Asn Thr Val Val Tyr Thr Ala Gln Gly Gly Tyr Tyr Ala Val Met Val
 1330 1335 1340
 Val Val Asp Gly Lys Ser Tyr Val Glu Lys Leu Ala Ile Lys
 1345 1350 1355

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8640 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 971..6031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGCCTTTGA GACGGGCACA AGCCGCCGCA GCCTCCTCTT CGAAGGTGTC TCGAACGTCC	60
ACATCGGTGA ATCCGTAGCA GTGCTCATTG CCATTGAGCA GCACCGAGGT GTGGCGCATC	120
AGATATATTT TCATCAGTGG ATTATTAGGG TATCGGTCAG AAAAAGCCTT CCGAATCCGA	180
CAAAGATAGT AGAAAGAGAG TGCATCTGAA AACAGATCAT TCGAGGATTA TCGATCAACT	240
GAAAAGGCAG GAGTTGTTTT GCGTTTTGGT TCGGAAAATT ACCTGATCAG CATTCGTAAA	300

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AACGTGGCGC GAGAATTTT TCGTTTGGC GCGAGAATTA AAAATTTTGG GAACCCACAGC	360
GAAAAAATC TCGCGCCGTT TTCTCAGGAT TTACAGACCA CAATCCGAGC ATTTTCGGTT	420
CGTAATTCAT CGAAGAGACA GGTTTTACCG CATTGAAATC AGAGAGAGAA TATCCGTAGT	480
CCAACGGTTC ATCCTTATAT CAGAGGTTAA AAGATATGGT ACGCTCATCG AGGAGCTGAT	540
TGGCTTAGTA GGTGAGACTT TCTTAAGAGA CTATCGGCAC CTACAGGAAG TTCATGGCAC	600
ACAAGGCAAA GGAGGCAATC TTCGCAGACC GGACTCATAT CAAAAGGATG AAACGACTTT	660
TCCATACGAC AACCAATAG CCGTCTACGG TAGACGAATG CAAACCCAAT ATGAGGCCAT	720
CAATCAATCC GAATGACAGC TTTTGGGCAA TATATTATGC ATATTTTGAT TCGCGTTTAA	780
AGGAAAAGTG CATATATTG CGATTGTGGT ATTTCTTTCG GTTCTATGT GAATTTTGTC	840
TCCCAAGRAG ACTTTATAAT GCATAAATAC AGAAGGGGTA CTACACAGTA AAATCATATT	900
CTAATTTTCAT CAAAATGAAA AACTTGAACA AGTTTGTTTC ATTGCTCTTT GCTCTTCTT	960
ATTAGGAGGA ATG GCA TTT GCG CAG CAG ACA GAG TTG GGA CGC AAT CCG	1009
Met Ala Phe Ala Gln Gln Thr Glu Leu Gly Arg Asn Pro	
1360 1365 1370	
AAT GTC AGA TTG CTC GAA TCC ACT CAG CAA TCG GTG ACA AAG GTT CAG	1057
Asn Val Arg Leu Leu Glu Ser Thr Gln Gln Ser Val Thr Lys Val Gln	
1375 1380 1385	
TTC CGT ATG GAC AAC CTC AAG TTC ACC GAA GTT CAA ACC CCT AAG GGA	1105
Phe Arg Met Asp Asn Leu Lys Phe Thr Glu Val Gln Thr Pro Lys Gly	
1390 1395 1400	
ATG GCA CAA GTG CCG ACC TAT ACA GAA GGG GTT AAT CTT TCC GAA AAA	1153
Met Ala Gln Val Pro Thr Tyr Thr Glu Gly Val Asn Leu Ser Glu Lys	
1405 1410 1415 1420	
GGG ATG CCT ACG CTT CCC ATT CTA TCA CGC TCT TTG GCG GTT TCA GAC	1201
Gly Met Pro Thr Leu Pro Ile Leu Ser Arg Ser Leu Ala Val Ser Asp	
1425 1430 1435	
ACT CGT GAG ATG AAG GTA GAG GTT GTT TCC TCA AAG TTC ATC GAA AAG	1249
Thr Arg Glu Met Lys Val Glu Val Val Ser Ser Lys Phe Ile Glu Lys	
1440 1445 1450	
AAA AAT GTC CTG ATT GCA CCC TCC AAG GGC ATG ATT ATG CGT AAC GAA	1297
Lys Asn Val Leu Ile Ala Pro Ser Lys Gly Met Ile Met Arg Asn Glu	
1455 1460 1465	
GAT CCG AAA AAG ATC CCT TAC GTT TAT GGA AAG AGC TAC TCG CAA AAC	1345
Asp Pro Lys Lys Ile Pro Tyr Val Tyr Gly Lys Ser Tyr Ser Gln Asn	
1470 1475 1480	
AAA TTC TTC CCG GGA GAG ATC GCC ACG CTT GAT GAT CCT TTT ATC CTT	1393
Lys Phe Phe Pro Gly Glu Ile Ala Thr Leu Asp Asp Pro Phe Ile Leu	
1485 1490 1495 1500	
CGT GAT GTG CGT GGA CAG GTT GTA AAC TTT GCG CCT TTG CAG TAT AAC	1441
Arg Asp Val Arg Gly Gln Val Val Asn Phe Ala Pro Leu Gln Tyr Asn	
1505 1510 1515	

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CCT GTG ACA AAG ACG TTG CGC ATC TAT ACG GAA ATC ACT GTG GCA GTG Pro Val Thr Lys Thr Leu Arg Ile Tyr Thr Glu Ile Thr Val Ala Val 1520 1525 1530	1489
AGC GAA ACT TCG GAA CAA GGC AAA AAT ATT CTG AAC AAG AAA GGT ACA Ser Glu Thr Ser Glu Gln Gly Lys Asn Ile Leu Asn Lys Lys Gly Thr 1535 1540 1545	1537
TTT GCC GGC TTT GAA GAC ACA TAC AAG CGC ATG TTC ATG AAC TAC GAG Phe Ala Gly Phe Glu Asp Thr Tyr Lys Arg Met Phe Met Asn Tyr Glu 1550 1555 1560	1585
CCG GGG CGT TAC ACA CCG GTA GAG GAA AAA CAA AAT GGT CGT ATG ATC Pro Gly Arg Tyr Thr Pro Val Glu Glu Lys Gln Asn Gly Arg Met Ile 1565 1570 1575 1580	1633
GTC ATC GTA GCC AAA AAG TAT GAG GGA GAT ATT AAA GAT TTC GTT GAT Val Ile Val Ala Lys Lys Tyr Glu Gly Asp Ile Lys Asp Phe Val Asp 1585 1590 1595	1681
TGG AAA AAC CAA CGC GGT CTC CGT ACC GAG GTG AAA GTG GCA GAA GAT Trp Lys Asn Gln Arg Gly Leu Arg Thr Glu Val Lys Val Ala Glu Asp 1600 1605 1610	1729
ATT GCT TCT CCC GTT ACA GCT AAT GCT ATT CAG CAG TTC GTT AAG CAA Ile Ala Ser Pro Val Thr Ala Asn Ala Ile Gln Gln Phe Val Lys Gln 1615 1620 1625	1777
GAA TAC GAG AAA GAA GGT AAT GAT TTG ACC TAT GTT CTT TTG GTT GGC Glu Tyr Glu Lys Glu Gly Asn Asp Leu Thr Tyr Val Leu Leu Val Gly 1630 1635 1640	1825
GAT CAC AAA GAT ATT CCT GCC AAA ATT ACT CCG GGG ATC AAA TCC GAC Asp His Lys Asp Ile Pro Ala Lys Ile Thr Pro Gly Ile Lys Ser Asp 1645 1650 1655 1660	1873
CAG GTA TAT GGA CAA ATA GTA GGT AAT GAC CAC TAC AAC GAA GTC TTC Gln Val Tyr Gly Gln Ile Val Gly Asn Asp His Tyr Asn Glu Val Phe 1665 1670 1675	1921
ATC GGT CGT TTC TCA TGT GAG AGC AAA GAG GAT CTG AAG ACA CAA ATC Ile Gly Arg Phe Ser Cys Glu Ser Lys Glu Asp Leu Lys Thr Gln Ile 1680 1685 1690	1969
GAT CGG ACT ATT CAC TAT GAG CGC AAT ATA ACC ACG GAA GAC AAA TGG Asp Arg Thr Ile His Tyr Glu Arg Asn Ile Thr Thr Glu Asp Lys Trp 1695 1700 1705	2017
CTC GGT CAG GCT CTT TGT ATT GCT TCG GCT GAA GGA GGC CCA TCC GCA Leu Gly Gln Ala Leu Cys Ile Ala Ser Ala Glu Gly Gly Pro Ser Ala 1710 1715 1720	2065
GAC AAT GGT GAA AGT GAT ATC CAG CAT GAG AAT GTA ATC GCC AAT CTG Asp Asn Gly Glu Ser Asp Ile Gln His Glu Asn Val Ile Ala Asn Leu 1725 1730 1735 1740	2113
CTT ACC CAG TAT GGC TAT ACC AAG ATT ATC AAA TGT TAT GAT CCG GGA Leu Thr Gln Tyr Gly Tyr Thr Lys Ile Ile Lys Cys Tyr Asp Pro Gly 1745 1750 1755	2161
GTA ACT CCT AAA AAC ATT ATT GAT GCT TTC AAC GGA GGA ATC TCG TTG Val Thr Pro Lys Asn Ile Ile Asp Ala Phe Asn Gly Gly Ile Ser Leu 1760 1765 1770	2209

GTC AAC TAT ACG GGC CAC GGT AGC GAA ACA GCT TGG GGT ACG TCT CAC Val Asn Tyr Thr Gly His Gly Ser Glu Thr Ala Trp Gly Thr Ser His 1775 1780 1785	2257
TTC GGC ACC ACT CAT GTG AAG CAG CTT ACC AAC AGC AAC CAG CTA CCG Phe Gly Thr Thr His Val Lys Gln Leu Thr Asn Ser Asn Gln Leu Pro 1790 1795 1800	2305
TTT ATT TTC GAC GTA GCT TGT GTG AAT GGC GAT TTC CTA TTC AGC ATG Phe Ile Phe Asp Val Ala Cys Val Asn Gly Asp Phe Leu Phe Ser Met 1805 1810 1815 1820	2353
CCT TGC TTC GCA GAA GCC CTG ATG CGT GCA CAA AAA GAT GGT AAG CCG Pro Cys Phe Ala Glu Ala Leu Met Arg Ala Gln Lys Asp Gly Lys Pro 1825 1830 1835	2401
ACA GGT ACT GTT GCT ATC ATA GCG TCT ACG ATC AAC CAG TCT TGG GCT Thr Gly Thr Val Ala Ile Ile Ala Ser Thr Ile Asn Gln Ser Trp Ala 1840 1845 1850	2449
TCT CCT ATG CGC GGG CAG GAT GAG ATG AAC GAA ATT CTG TGC GAA AAA Ser Pro Met Arg Gly Gln Asp Glu Met Asn Glu Ile Leu Cys Glu Lys 1855 1860 1865	2497
CAC CCG AAC AAC ATC AAG CGT ACT TTC GGT GGT GTC ACC ATG AAC GGT His Pro Asn Asn Ile Lys Arg Thr Phe Gly Gly Val Thr Met Asn Gly 1870 1875 1880	2545
ATG TTT GCT ATG GTG GAA AAG TAT AAA AAG GAT GGT GAG AAG ATG CTC Met Phe Ala Met Val Glu Lys Tyr Lys Lys Asp Gly Glu Lys Met Leu 1885 1890 1895 1900	2593
GAC ACA TGG ACT GTT TTC GGC GAC CCC TCG CTG CTC GTT CGT ACA CTT Asp Thr Trp Thr Val Phe Gly Asp Pro Ser Leu Leu Val Arg Thr Leu 1905 1910 1915	2641
GTC CCG ACC AAA ATG CAG GTT ACG GCT CCG GCT CAG ATT AAT TTG ACG Val Pro Thr Lys Met Gln Val Thr Ala Pro Ala Gln Ile Asn Leu Thr 1920 1925 1930	2689
GAT GCT TCA GTC AAC GTA TCT TGC GAT TAT AAT GGT GCT ATT GCT ACC Asp Ala Ser Val Asn Val Ser Cys Asp Tyr Asn Gly Ala Ile Ala Thr 1935 1940 1945	2737
ATT TCA GCC AAT GGA AAG ATG TTC GGT TCT GCA GTT GTC GAA AAT GGA Ile Ser Ala Asn Gly Lys Met Phe Gly Ser Ala Val Val Glu Asn Gly 1950 1955 1960	2785
ACA GCT ACA ATC AAT CTG ACA GGT CTG ACA AAT GAA AGC ACG CTT ACC Thr Ala Thr Ile Asn Leu Thr Gly Leu Thr Asn Glu Ser Thr Leu Thr 1965 1970 1975 1980	2833
CTT ACA GTA GTT GGT TAC AAC AAA GAG ACG GTT ATT AAG ACC ATC AAC Leu Thr Val Val Gly Tyr Asn Lys Glu Thr Val Ile Lys Thr Ile Asn 1985 1990 1995	2881
ACT AAT GGT GAG CCT AAC CCC TAC CAG CCC GTT TCC AAC TTG ACA GCT Thr Asn Gly Glu Pro Asn Pro Tyr Gln Pro Val Ser Asn Leu Thr Ala 2000 2005 2010	2929
ACA ACG CAG GGT CAG AAA GTA ACG CTC AAG TGG GAT GCA CCG AGC ACG Thr Thr Gln Gly Gln Lys Val Thr Leu Lys Trp Asp Ala Pro Ser Thr 2015 2020 2025	2977

AAA ACC AAT GCA ACC ACT AAT ACC GCT CGC AGC GTG GAT GGC ATA CGA Lys Thr Asn Ala Thr Thr Asn Thr Ala Arg Ser Val Asp Gly Ile Arg 2030 2035 2040	3025
GAA TTG GTT CTT CTG TCA GTC AGC GAT GCC CCC GAA CTT CTT CGC AGC Glu Leu Val Leu Leu Ser Val Ser Asp Ala Pro Glu Leu Leu Arg Ser 2045 2050 2055 2060	3073
GGT CAG GCC GAG ATT GTT CTT GAA GCT CAC GAT GTT TGG AAT GAT GGA Gly Gln Ala Glu Ile Val Leu Glu Ala His Asp Val Trp Asn Asp Gly 2065 2070 2075	3121
TCC GGT TAT CAG ATT CTT TTG GAT GCA GAC CAT GAT CAA TAT GGA CAG Ser Gly Tyr Gln Ile Leu Leu Asp Ala Asp His Asp Gln Tyr Gly Gln 2080 2085 2090	3169
GTT ATA CCC AGT GAT ACC CAT ACT CTT TGG CCG AAC TGT AGT GTC CCG Val Ile Pro Ser Asp Thr His Thr Leu Trp Pro Asn Cys Ser Val Pro 2095 2100 2105	3217
GCC AAT CTG TTC GCT CCG TTC GAA TAT ACT GTT CCG GAA AAT GCA GAT Ala Asn Leu Phe Ala Pro Phe Glu Tyr Thr Val Pro Glu Asn Ala Asp 2110 2115 2120	3265
CCT TCT TGT TCC CCT ACC AAT ATG ATA ATG GAT GGT ACT GCA TCC GTT Pro Ser Cys Ser Pro Thr Asn Met Ile Met Asp Gly Thr Ala Ser Val 2125 2130 2135 2140	3313
AAT ATA CCG GCC GGA ACT TAT GAC TTT GCA ATT GCT GCT CCT CAA GCA Asn Ile Pro Ala Gly Thr Tyr Asp Phe Ala Ile Ala Ala Pro Gln Ala 2145 2150 2155	3361
AAT GCA AAG ATT TGG ATT GCC GGA CAA GGA CCG ACG AAA GAA GAT GAT Asn Ala Lys Ile Trp Ile Ala Gly Gln Gly Pro Thr Lys Glu Asp Asp 2160 2165 2170	3409
TAT GTA TTT GAA GCC GGT AAA AAA TAC CAT TTC CTT ATG AAG AAG ATG Tyr Val Phe Glu Ala Gly Lys Lys Tyr His Phe Leu Met Lys Lys Met 2175 2180 2185	3457
GGT AGC GGT GAT GGA ACT GAA TTG ACT ATA AGC GAA GGT GGT GGA AGC Gly Ser Gly Asp Gly Thr Glu Leu Thr Ile Ser Glu Gly Gly Gly Ser 2190 2195 2200	3505
GAT TAC ACC TAT ACT GTC TAT CGT GAC GGC ACG AAG ATC AAG GAA GGT Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Thr Lys Ile Lys Glu Gly 2205 2210 2215 2220	3553
CTG ACG GCT ACG ACA TTC GAA GAA GAC GGT GTA GCT ACG GGC AAT CAT Leu Thr Ala Thr Thr Phe Glu Glu Asp Gly Val Ala Thr Gly Asn His 2225 2230 2235	3601
GAG TAT TGC GTG GAA GTT AAG TAC ACA GCC GGC GTA TCT CCG AAG GTA Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Val 2240 2245 2250	3649
TGT AAA GAC GTT ACG GTA GAA GGA TCC AAT GAA TTT GCT CCT GTA CAG Cys Lys Asp Val Thr Val Glu Gly Ser Asn Glu Phe Ala Pro Val Gln 2255 2260 2265	3697
AAC CTG ACC GGT AGT GCA GTC GGC CAG AAA GTA ACG CTC AAG TGG GAT Asn Leu Thr Gly Ser Ala Val Gly Gln Lys Val Thr Leu Lys Trp Asp 2270 2275 2280	3745

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GCA CCT AAT GGT ACC CCG AAT CCA AAT CCG AAT CCG AAT CCG AAT CCG Ala Pro Asn Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn Pro Asn Pro 2285 2290 2295 2300	3793
AAT CCC GGA ACA ACA ACA CTT TCC GAA TCA TTC GAA AAT GGT ATT CCT Asn Pro Gly Thr Thr Thr Leu Ser Glu Ser Phe Glu Asn Gly Ile Pro 2305 2310 2315	3841
GCC TCA TGG AAG ACG ATC GAT GCA GAC GGT GAC GGG CAT GGC TGG AAG Ala Ser Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly His Gly Trp Lys 2320 2325 2330	3889
CCT GGA AAT GCT CCC GGA ATC GCT GGC TAC AAT AGC AAT GGT TGT GTA Pro Gly Asn Ala Pro Gly Ile Ala Gly Tyr Asn Ser Asn Gly Cys Val 2335 2340 2345	3937
TAT TCA GAG TCA TTC GGT CTT GGT GGT ATA GGA GTT CTT ACC CCT GAC Tyr Ser Glu Ser Phe Gly Leu Gly Gly Ile Gly Val Leu Thr Pro Asp 2350 2355 2360	3985
AAC TAT CTG ATA ACA CCG GCA TTG GAT TTG CCT AAC GGA GGT AAG TTG Asn Tyr Leu Ile Thr Pro Ala Leu Asp Leu Pro Asn Gly Gly Lys Leu 2365 2370 2375 2380	4033
ACT TTC TGG GTA TGC GCA CAG GAT GCT AAT TAT GCA TCC GAG CAC TAT Thr Phe Trp Val Cys Ala Gln Asp Ala Asn Tyr Ala Ser Glu His Tyr 2385 2390 2395	4081
GCG GTG TAT GCA TCT TCG ACC GGT AAC GAT GCA TCC AAC TTC ACG AAT Ala Val Tyr Ala Ser Ser Thr Gly Asn Asp Ala Ser Asn Phe Thr Asn 2400 2405 2410	4129
GCT TTG TTG GAA GAG ACG ATT ACG GCA AAA GGT GTT CGC TCG CCG GAA Ala Leu Leu Glu Glu Thr Ile Thr Ala Lys Gly Val Arg Ser Pro Glu 2415 2420 2425	4177
GCT ATT CGT GGT CGT ATA CAG GGT ACT TGG CGC CAG AAG ACG GTA GAC Ala Ile Arg Gly Arg Ile Gln Gly Thr Trp Arg Gln Lys Thr Val Asp 2430 2435 2440	4225
CTT CCC GCA GGT ACG AAA TAT GTT GCT TTC CGT CAC TTC CAA AGC ACG Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Phe Gln Ser Thr 2445 2450 2455 2460	4273
GAT ATG TTC TAC ATC GAC CTT GAT GAG GTT GAG ATC AAG GCC AAC GGC Asp Met Phe Tyr Ile Asp Leu Asp Glu Val Glu Ile Lys Ala Asn Gly 2465 2470 2475	4321
AAG CGC GCA GAC TTC ACG GAA ACG TTC GAG TCT TCT ACT CAT GGA GAG Lys Arg Ala Asp Phe Thr Glu Thr Phe Glu Ser Ser Thr His Gly Glu 2480 2485 2490	4369
GCA CCG GCG GAA TGG ACT ACT ATC GAT GCC GAT GGC GAT GGT CAG GGT Ala Pro Ala Glu Trp Thr Thr Ile Asp Ala Asp Gly Asp Gly Gln Gly 2495 2500 2505	4417
TGG CTC TGT CTG TCT TCC GGA CAA TTG GAC TGG CTG ACA GCT CAT GGC Trp Leu Cys Leu Ser Ser Gly Gln Leu Asp Trp Leu Thr Ala His Gly 2510 2515 2520	4465
GGC ACC AAC GTA GTA GCC TCT TTC TCA TGG AAT GGA ATG GCT TTG AAT Gly Thr Asn Val Val Ala Ser Phe Ser Trp Asn Gly Met Ala Leu Asn 2525 2530 2535 2540	4513

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CCT GAT AAC TAT CTC ATC TCA AAG GAT GTT ACA GGC GCA ACG AAG GTA Pro Asp Asn Tyr Leu Ile Ser Lys Asp Val Thr Gly Ala Thr Lys Val 2545 2550 2555	4561
AAG TAC TAC TAT GCA GTC AAC GAC GGT TTT CCC GGG GAT CAC TAT GCG Lys Tyr Tyr Tyr Ala Val Asn Asp Gly Phe Pro Gly Asp His Tyr Ala 2560 2565 2570	4609
GTG ATG ATC TCC AAG ACG GGC ACG AAC GCC GGA GAC TTC ACG GTT GTT Val Met Ile Ser Lys Thr Gly Thr Asn Ala Gly Asp Phe Thr Val Val 2575 2580 2585	4657
TTC GAA GAA ACG CCT AAC GGA ATA AAT AAG GGC GGA GCA AGA TTC GGT Phe Glu Glu Thr Pro Asn Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly 2590 2595 2600	4705
CTT TCC ACG GAA GCC AAT GGC GCC AAA CCT CAA AGT GTA TGG ATC GAG Leu Ser Thr Glu Ala Asn Gly Ala Lys Pro Gln Ser Val Trp Ile Glu 2605 2610 2615 2620	4753
CGT ACG GTA GAT TTG CCT GCG GGC ACG AAG TAT GTT GCT TTC CGT CAC Arg Thr Val Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His 2625 2630 2635	4801
TAC AAT TGC TCG GAT TTG AAC TAC ATT CTT TTG GAT GAT ATT CAG TTC Tyr Asn Cys Ser Asp Leu Asn Tyr Ile Leu Leu Asp Asp Ile Gln Phe 2640 2645 2650	4849
ACC ATG GGT GGC AGC CCC ACC CCG ACC GAT TAT ACC TAC ACG GTG TAT Thr Met Gly Gly Ser Pro Thr Pro Thr Asp Tyr Thr Tyr Thr Val Tyr 2655 2660 2665	4897
CGT GAC GGT ACG AAG ATC AAG GAA GGT CTG ACC GAA ACG ACC TTC GAA Arg Asp Gly Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr Thr Phe Glu 2670 2675 2680	4945
GAA GAC GGC GTA GCT ACA GGC AAT CAT GAG TAT TGC GTG GAA GTG AAG Glu Asp Gly Val Ala Thr Gly Asn His Glu Tyr Cys Val Glu Val Lys 2685 2690 2695 2700	4993
TAC ACA GCC GGC GTA TCT CCG AAA GAG TGC GTA AAC GTA ACT ATT AAT Tyr Thr Ala Gly Val Ser Pro Lys Glu Cys Val Asn Val Thr Ile Asn 2705 2710 2715	5041
CCG ACT CAG TTC AAT CCT GTA AAG AAC CTG AAG GCA CAA CCG GAT GGC Pro Thr Gln Phe Asn Pro Val Lys Asn Leu Lys Ala Gln Pro Asp Gly 2720 2725 2730	5089
GGC GAC GTG GTT CTC AAG TGG GAA GCC CCG AGC GCA AAA AAG ACA GAA Gly Asp Val Val Leu Lys Trp Glu Ala Pro Ser Ala Lys Lys Thr Glu 2735 2740 2745	5137
GGT TCT CGT GAA GTA AAA CGG ATC GGA GAC GGT CTT TTC GTT ACG ATC Gly Ser Arg Glu Val Lys Arg Ile Gly Asp Gly Leu Phe Val Thr Ile 2750 2755 2760	5185
GAA CCT GCA AAC GAT GTA CGT GCC AAC GAA GCC AAG GTT GTG CTC GCA Glu Pro Ala Asn Asp Val Arg Ala Asn Glu Ala Lys Val Val Leu Ala 2765 2770 2775 2780	5233
GCA GAC AAC GTA TGG GGA GAC AAT ACG GGT TAC CAG TTC TTG TTG GAT Ala Asp Asn Val Trp Gly Asp Asn Thr Gly Tyr Gln Phe Leu Leu Asp 2785 2790 2795	5281

GCC GAT CAC AAT ACA TTC GGA AGT GTC ATT CCG GCA ACC GGT CCT CTC Ala Asp His Asn Thr Phe Gly Ser Val Ile Pro Ala Thr Gly Pro Leu 2800 2805 2810	5329
TTT ACC GGA ACA GCT TCT TCC AAT CTT TAC AGT GCG AAC TTC GAG TAT Phe Thr Gly Thr Ala Ser Ser Asn Leu Tyr Ser Ala Asn Phe Glu Tyr 2815 2820 2825	5377
TTG ATC CCG GCC AAT GCC GAT CCT GTT GTT ACT ACA CAG AAT ATT ATC Leu Ile Pro Ala Asn Ala Asp Pro Val Val Thr Thr Gln Asn Ile Ile 2830 2835 2840	5425
GTT ACA GGA CAG GGT GAA GTT GTA ATC CCC GGT GGT GTT TAC GAC TAT Val Thr Gly Gln Gly Glu Val Val Ile Pro Gly Gly Val Tyr Asp Tyr 2845 2850 2855 2860	5473
TGC ATT ACG AAC CCG GAA CCT GCA TCC GGA AAG ATG TGG ATC GCA GGA Cys Ile Thr Asn Pro Glu Pro Ala Ser Gly Lys Met Trp Ile Ala Gly 2865 2870 2875	5521
GAT GGA GGC AAC CAG CCT GCA CGT TAT GAC GAT TTC ACA TTC GAA GCA Asp Gly Gly Asn Gln Pro Ala Arg Tyr Asp Asp Phe Thr Phe Glu Ala 2880 2885 2890	5569
GGC AAG AAG TAC ACC TTC ACG ATG CGT CGC GCC GGA ATG GGA GAT GGA Gly Lys Lys Tyr Thr Phe Thr Met Arg Arg Ala Gly Met Gly Asp Gly 2895 2900 2905	5617
ACT GAT ATG GAA GTC GAA GAC GAT TCA CCT GCA AGC TAT ACC TAT ACA Thr Asp Met Glu Val Glu Asp Asp Ser Pro Ala Ser Tyr Thr Tyr Thr 2910 2915 2920	5665
GTC TAT CGT GAC GGC ACG AAG ATC AAG GAA GGT CTG ACC GAA ACG ACC Val Tyr Arg Asp Gly Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr Thr 2925 2930 2935 2940	5713
TAC CGC GAT GCA GGA ATG AGT GCA CAA TCT CAT GAG TAT TGC GTA GAG Tyr Arg Asp Ala Gly Met Ser Ala Gln Ser His Glu Tyr Cys Val Glu 2945 2950 2955	5761
GTT AAG TAC GCA GCC GGC GTA TCT CCG AAG GTT TGT GTG GAT TAT ATT Val Lys Tyr Ala Ala Gly Val Ser Pro Lys Val Cys Val Asp Tyr Ile 2960 2965 2970	5809
CCT GAC GGA GTG GCA GAC GTA ACG GCT CAG AAG CCT TAC ACG CTG ACA Pro Asp Gly Val Ala Asp Val Thr Ala Gln Lys Pro Tyr Thr Leu Thr 2975 2980 2985	5857
GTT GTT GGA AAG ACG ATC ACG GTA ACT TGC CAA GGC GAA GCT ATG ATC Val Val Gly Lys Thr Ile Thr Val Thr Cys Gln Gly Glu Ala Met Ile 2990 2995 3000	5905
TAC GAC ATG AAC GGT CGT CGT CTG GCA GCC GGT CGC AAC ACA GTT GTT Tyr Asp Met Asn Gly Arg Arg Leu Ala Ala Gly Arg Asn Thr Val Val 3005 3010 3015 3020	5953
TAC ACG GCT CAG GGC GGC TAC TAT GCA GTC ATG GTT GTC GTT GAC GGC Tyr Thr Ala Gln Gly Gly Tyr Tyr Ala Val Met Val Val Val Asp Gly 3025 3030 3035	6001
AAG TCT TAC GTA GAG AAA CTC GCT GTA AAG TAATTCTGTC TTGGACTCGG Lys Ser Tyr Val Glu Lys Leu Ala Val Lys 3040 3045	6051

AGACTTTGTG CAGACACTTT TAATATAGGT CTGTAATTGT CTCAGAGTAT GAATCGATCG	6111
CCCGACCTCC TTTTAAGGAA GTCGGGCGAC TTCGTTTTTA TGCCTATTAT TCTAATATAC	6171
TTCTGAAACA ATTTGTTCCA AAAAGTTGCA TGAAAAGATT ATCTTACTAT CTTTGCACTG	6231
CAAAAGGGGA GTTTCCTAAG GTTTTCCCCG GAGTAGTACG GTAATAACGG TGTGGTAGTT	6291
CAGCTGGTTA GAATACCTGC CTGTCACGCA GGGGGTCGCG GGTTTCGAGTC CCGTCCATAC	6351
CGCTAAAATA AGGAGTTGTG TTGAAATAGT TTTTCGGCAC AGCTCCATTT TTGTATGTTA	6411
TCGCAGCACC GGAAAGTATA ATTGCCGGAT GAGATTATTC AATATGCTCG GAAGATTTTC	6471
TTAGAACGAA GCAGAAGTGT TTGTCTTTAT TACGATCTGC TTGGGACATA GGGATTAAAT	6531
TAGTATTATT GCAGGAGGGA CGGTACATGG AGTCGCCCCG CCAATCAGAT GAAGAAAGAA	6591
GAAGTACGAT TGATTTTTAT GGGAACGGCC GATTTTGCTG TTCCGGCACT CCGAGCTTTG	6651
GTCGAAAACG GATACCAAGT AAAAGCTGTG GTCACTATGC CGGACAAGCC TATGGGTCGA	6711
GGACATAAGG TAAGTCCCAG TATGGTCAAA CTATACGCAC AGGAATTGGG TCTGCCTATT	6771
CTCCAGCCGG ACAATCTGAA CGAGGAATCT TTTCTCGATG AACTACGGAC TTATCAGCCG	6831
CAGTTGCAAA TCGTAGTGGC TTTCCGTATG CTTCTCGCT CCGTATGGCA AATGCCCCC	6891
ATGGGAACAA TCAATCTGCA TGGCTCTCTG CTGCCCATGT ATCGAGGAGC AGCCCCATC	6951
AACCACGCGA TACGCCATGG CGATACGGAA ACGGGAGTTA CCACCTCCG CCTCCGGCAT	7011
GAGATAGATA CGGGTGAAGT ACTGCTGCAA GAGAAGTTGC CTATAGGACA TGAAGAGACT	7071
TTCCGGCAAT TGTACGAACG TATGGCTACT CTCGGTGCAT CCGTATTGGT GCACACAGTG	7131
GACTTGTTTC TCGAAGGAGA ACCCGTCTCC ATACCACAGG AGCAACTTCC GGGCTATGTT	7191
GGTGCTCGAC CGGCTCCGAA GATTTTCAAA GACGACTGCC GTATCGATTG GGACAAACCG	7251
GCTGAAGAGG TACACAATTT CATCCGAGC ATATCGCCTG CCCCTACAGC TTGGACCAAG	7311
CTTCATCGTC CAGGGATGGA GTCCATCGTG CTGAAAATAT ACCGTACCCA AGTGATAGAA	7371
CGAGAACCGC GACACAGAGG CCGATTCCGC TCCATCATAT GGGACAAGAA AAACCTCGAC	7431
GTGATGACCC GCAAAGGGGT CATACGTATA CTCTCGCTCC AAATGCCCGG CAAGAAACAA	7491
ATGGATGCTG CCTCTTTCCT CAATGGTTTC GCTTTGCTCT CAGATATGTA TATAGAATAG	7551
GAGAGAGCTT GTTCCAAGGT TTGAACTGCT CATTTTCTGA CCTCTGCAAT ACAATAACAA	7611
TGTGCGGAGG ATACTTCTCT GCTCAACGTT CAGAGAAGCA GTTGGTCGTA GGCCGAGCCA	7671
ATCACATGGT TTTTAACTT TGTAACCGAA AAATAACGA CATCATGAAA GAAAACGAAA	7731
AGCCGACAGC TGCTGCCGGA ACCGTAACCA CCACCGATAA GACAAAGCCT GATTGGCGCA	7791
AAATCCTACC TTATGCTGCG GTCGTAATCC TTTTCATAGC CCTCGCTTTG GCCTATTTCT	7851
ATCCCGCCTC ATTCGACGGG CGTGTACTGT TCCAGGGCGA CGTAGCGGGA GCCAGCGGTA	7911
CGGCGCAGGA CGTACGCGAT TGGGAGGCAC AGACAGGAGA AACTCCTAT TGGACCAACA	7971

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GTCTCTTCGG GGGGATGCCT ATGTACCAGA TTTCGCCAAG CTATCCCTCT ACCCATACGC 8031
 TCCAAACCAT ACAGGATGTT CTGACCCTGC GCAAGCCTTT CTATCTATTA GGCACCTATG 8091
 CCTGGATGCT TTTTGCCATG ATGGGAGGGT TCTTTCTTTT CCTTAGATCG CTTCGAATCA 8151
 GGATTTTGCC GGCAGTCATA GGCTCCATCG CATGGGCCCTT TTCTTCCTAC TTCCTGATTC 8211
 TGATTATGGC CGGACATATA TGAAGCTGA CAGCTATGTG TTTTATTCCT CCTACTCTTG 8271
 CCGGTATGAT CTGGATCTAC AATGGGAGGT GGTGGCAGG CGGTAGCGTG ATGGCTTTTT 8331
 TCACGGCTTT GCAAGTCTTG GCTAATCATG TACAGATGAG CTATTACTTC CTGTTTCGTCA 8391
 TGTTTTTCAT GGTGTTGGCT TTCTTGGCAG AAGCCATTCA AACAAAACGA ATCCGACACT 8451
 TCTTCCTTTC CTCGGCAGTA GTCGTCATAG CAGGTCTGGT GGGTATAGCT GTGAATAGTA 8511
 CCAACCTCTT CCACACCTAC CAATACGGCA AAGAGACCAT GCGTGGAGGT AGCGAACTGA 8571
 CGCTCAAGCA GAGCGGAGCA CCCACGGATC AAGTGACGCA TGAGAATAAA AGCGGACTGG 8631
 ACAAGGCCT 8640

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1687 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ala Phe Ala Gln Gln Thr Glu Leu Gly Arg Asn Pro Asn Val Arg
 1 5 10 15
 Leu Leu Glu Ser Thr Gln Gln Ser Val Thr Lys Val Gln Phe Arg Met
 20 25 30
 Asp Asn Leu Lys Phe Thr Glu Val Gln Thr Pro Lys Gly Met Ala Gln
 35 40 45
 Val Pro Thr Tyr Thr Glu Gly Val Asn Leu Ser Glu Lys Gly Met Pro
 50 55 60
 Thr Leu Pro Ile Leu Ser Arg Ser Leu Ala Val Ser Asp Thr Arg Glu
 65 70 75 80
 Met Lys Val Glu Val Val Ser Ser Lys Phe Ile Glu Lys Lys Asn Val
 85 90 95
 Leu Ile Ala Pro Ser Lys Gly Met Ile Met Arg Asn Glu Asp Pro Lys
 100 105 110
 Lys Ile Pro Tyr Val Tyr Gly Lys Ser Tyr Ser Gln Asn Lys Phe Phe
 115 120 125
 Pro Gly Glu Ile Ala Thr Leu Asp Asp Pro Phe Ile Leu Arg Asp Val
 130 135 140

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Arg Gly Gln Val Val Asn Phe Ala Pro Leu Gln Tyr Asn Pro Val Thr
 145 150 155 160
 Lys Thr Leu Arg Ile Tyr Thr Glu Ile Thr Val Ala Val Ser Glu Thr
 165 170 175
 Ser Glu Gln Gly Lys Asn Ile Leu Asn Lys Lys Gly Thr Phe Ala Gly
 180 185 190
 Phe Glu Asp Thr Tyr Lys Arg Met Phe Met Asn Tyr Glu Pro Gly Arg
 195 200 205
 Tyr Thr Pro Val Glu Glu Lys Gln Asn Gly Arg Met Ile Val Ile Val
 210 215 220
 Ala Lys Lys Tyr Glu Gly Asp Ile Lys Asp Phe Val Asp Trp Lys Asn
 225 230 235 240
 Gln Arg Gly Leu Arg Thr Glu Val Lys Val Ala Glu Asp Ile Ala Ser
 245 250 255
 Pro Val Thr Ala Asn Ala Ile Gln Gln Phe Val Lys Gln Glu Tyr Glu
 260 265 270
 Lys Glu Gly Asn Asp Leu Thr Tyr Val Leu Leu Val Gly Asp His Lys
 275 280 285
 Asp Ile Pro Ala Lys Ile Thr Pro Gly Ile Lys Ser Asp Gln Val Tyr
 290 295 300
 Gly Gln Ile Val Gly Asn Asp His Tyr Asn Glu Val Phe Ile Gly Arg
 305 310 315 320
 Phe Ser Cys Glu Ser Lys Glu Asp Leu Lys Thr Gln Ile Asp Arg Thr
 325 330 335
 Ile His Tyr Glu Arg Asn Ile Thr Thr Glu Asp Lys Trp Leu Gly Gln
 340 345 350
 Ala Leu Cys Ile Ala Ser Ala Glu Gly Gly Pro Ser Ala Asp Asn Gly
 355 360 365
 Glu Ser Asp Ile Gln His Glu Asn Val Ile Ala Asn Leu Leu Thr Gln
 370 375 380
 Tyr Gly Tyr Thr Lys Ile Ile Lys Cys Tyr Asp Pro Gly Val Thr Pro
 385 390 395 400
 Lys Asn Ile Ile Asp Ala Phe Asn Gly Gly Ile Ser Leu Val Asn Tyr
 405 410 415
 Thr Gly His Gly Ser Glu Thr Ala Trp Gly Thr Ser His Phe Gly Thr
 420 425 430
 Thr His Val Lys Gln Leu Thr Asn Ser Asn Gln Leu Pro Phe Ile Phe
 435 440 445
 Asp Val Ala Cys Val Asn Gly Asp Phe Leu Phe Ser Met Pro Cys Phe
 450 455 460
 Ala Glu Ala Leu Met Arg Ala Gln Lys Asp Gly Lys Pro Thr Gly Thr
 465 470 475 480

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Val Ala Ile Ile Ala Ser Thr Ile Asn Gln Ser Trp Ala Ser Pro Met
 485 490 495
 Arg Gly Gln Asp Glu Met Asn Glu Ile Leu Cys Glu Lys His Pro Asn
 500 505 510
 Asn Ile Lys Arg Thr Phe Gly Gly Val Thr Met Asn Gly Met Phe Ala
 515 520 525
 Met Val Glu Lys Tyr Lys Lys Asp Gly Glu Lys Met Leu Asp Thr Trp
 530 535 540
 Thr Val Phe Gly Asp Pro Ser Leu Leu Val Arg Thr Leu Val Pro Thr
 545 550 555 560
 Lys Met Gln Val Thr Ala Pro Ala Gln Ile Asn Leu Thr Asp Ala Ser
 565 570 575
 Val Asn Val Ser Cys Asp Tyr Asn Gly Ala Ile Ala Thr Ile Ser Ala
 580 585 590
 Asn Gly Lys Met Phe Gly Ser Ala Val Val Glu Asn Gly Thr Ala Thr
 595 600 605
 Ile Asn Leu Thr Gly Leu Thr Asn Glu Ser Thr Leu Thr Leu Thr Val
 610 615 620
 Val Gly Tyr Asn Lys Glu Thr Val Ile Lys Thr Ile Asn Thr Asn Gly
 625 630 635 640
 Glu Pro Asn Pro Tyr Gln Pro Val Ser Asn Leu Thr Ala Thr Thr Gln
 645 650 655
 Gly Gln Lys Val Thr Leu Lys Trp Asp Ala Pro Ser Thr Lys Thr Asn
 660 665 670
 Ala Thr Thr Asn Thr Ala Arg Ser Val Asp Gly Ile Arg Glu Leu Val
 675 680 685
 Leu Leu Ser Val Ser Asp Ala Pro Glu Leu Leu Arg Ser Gly Gln Ala
 690 695 700
 Glu Ile Val Leu Glu Ala His Asp Val Trp Asn Asp Gly Ser Gly Tyr
 705 710 715 720
 Gln Ile Leu Leu Asp Ala Asp His Asp Gln Tyr Gly Gln Val Ile Pro
 725 730 735
 Ser Asp Thr His Thr Leu Trp Pro Asn Cys Ser Val Pro Ala Asn Leu
 740 745 750
 Phe Ala Pro Phe Glu Tyr Thr Val Pro Glu Asn Ala Asp Pro Ser Cys
 755 760 765
 Ser Pro Thr Asn Met Ile Met Asp Gly Thr Ala Ser Val Asn Ile Pro
 770 775 780
 Ala Gly Thr Tyr Asp Phe Ala Ile Ala Ala Pro Gln Ala Asn Ala Lys
 785 790 795 800
 Ile Trp Ile Ala Gly Gln Gly Pro Thr Lys Glu Asp Asp Tyr Val Phe
 805 810 815

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Glu Ala Gly Lys Lys Tyr His Phe Leu Met Lys Lys Met Gly Ser Gly
 820 825 830

Asp Gly Thr Glu Leu Thr Ile Ser Glu Gly Gly Gly Ser Asp Tyr Thr
 835 840 845

Tyr Thr Val Tyr Arg Asp Gly Thr Lys Ile Lys Glu Gly Leu Thr Ala
 850 855 860

Thr Thr Phe Glu Glu Asp Gly Val Ala Thr Gly Asn His Glu Tyr Cys
 865 870 875 880

Val Glu Val Lys Tyr Thr Ala Gly Val Ser Pro Lys Val Cys Lys Asp
 885 890 895

Val Thr Val Glu Gly Ser Asn Glu Phe Ala Pro Val Gln Asn Leu Thr
 900 905 910

Gly Ser Ala Val Gly Gln Lys Val Thr Leu Lys Trp Asp Ala Pro Asn
 915 920 925

Gly Thr Pro Asn Pro Asn Pro Asn Pro Asn Pro Asn Pro Asn Pro Gly
 930 935 940

Thr Thr Thr Leu Ser Glu Ser Phe Glu Asn Gly Ile Pro Ala Ser Trp
 945 950 955 960

Lys Thr Ile Asp Ala Asp Gly Asp Gly His Gly Trp Lys Pro Gly Asn
 965 970 975

Ala Pro Gly Ile Ala Gly Tyr Asn Ser Asn Gly Cys Val Tyr Ser Glu
 980 985 990

Ser Phe Gly Leu Gly Gly Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu
 995 1000 1005

Ile Thr Pro Ala Leu Asp Leu Pro Asn Gly Gly Lys Leu Thr Phe Trp
 1010 1015 1020

Val Cys Ala Gln Asp Ala Asn Tyr Ala Ser Glu His Tyr Ala Val Tyr
 1025 1030 1035 1040

Ala Ser Ser Thr Gly Asn Asp Ala Ser Asn Phe Thr Asn Ala Leu Leu
 1045 1050 1055

Glu Glu Thr Ile Thr Ala Lys Gly Val Arg Ser Pro Glu Ala Ile Arg
 1060 1065 1070

Gly Arg Ile Gln Gly Thr Trp Arg Gln Lys Thr Val Asp Leu Pro Ala
 1075 1080 1085

Gly Thr Lys Tyr Val Ala Phe Arg His Phe Gln Ser Thr Asp Met Phe
 1090 1095 1100

Tyr Ile Asp Leu Asp Glu Val Glu Ile Lys Ala Asn Gly Lys Arg Ala
 1105 1110 1115 1120

Asp Phe Thr Glu Thr Phe Glu Ser Ser Thr His Gly Glu Ala Pro Ala
 1125 1130 1135

Glu Trp Thr Thr Ile Asp Ala Asp Gly Asp Gly Gln Gly Trp Leu Cys
 1140 1145 1150

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Leu Ser Ser Gly Gln Leu Asp Trp Leu Thr Ala His Gly Gly Thr Asn
 1155 1160 1165
 Val Val Ala Ser Phe Ser Trp Asn Gly Met Ala Leu Asn Pro Asp Asn
 1170 1175 1180
 Tyr Leu Ile Ser Lys Asp Val Thr Gly Ala Thr Lys Val Lys Tyr Tyr
 1185 1190 1195 1200
 Tyr Ala Val Asn Asp Gly Phe Pro Gly Asp His Tyr Ala Val Met Ile
 1205 1210 1215
 Ser Lys Thr Gly Thr Asn Ala Gly Asp Phe Thr Val Val Phe Glu Glu
 1220 1225 1230
 Thr Pro Asn Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly Leu Ser Thr
 1235 1240 1245
 Glu Ala Asn Gly Ala Lys Pro Gln Ser Val Trp Ile Glu Arg Thr Val
 1250 1255 1260
 Asp Leu Pro Ala Gly Thr Lys Tyr Val Ala Phe Arg His Tyr Asn Cys
 1265 1270 1275 1280
 Ser Asp Leu Asn Tyr Ile Leu Leu Asp Asp Ile Gln Phe Thr Met Gly
 1285 1290 1295
 Gly Ser Pro Thr Pro Thr Asp Tyr Thr Tyr Thr Val Tyr Arg Asp Gly
 1300 1305 1310
 Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr Thr Phe Glu Glu Asp Gly
 1315 1320 1325
 Val Ala Thr Gly Asn His Glu Tyr Cys Val Glu Val Lys Tyr Thr Ala
 1330 1335 1340
 Gly Val Ser Pro Lys Glu Cys Val Asn Val Thr Ile Asn Pro Thr Gln
 1345 1350 1355 1360
 Phe Asn Pro Val Lys Asn Leu Lys Ala Gln Pro Asp Gly Gly Asp Val
 1365 1370 1375
 Val Leu Lys Trp Glu Ala Pro Ser Ala Lys Lys Thr Glu Gly Ser Arg
 1380 1385 1390
 Glu Val Lys Arg Ile Gly Asp Gly Leu Phe Val Thr Ile Glu Pro Ala
 1395 1400 1405
 Asn Asp Val Arg Ala Asn Glu Ala Lys Val Val Leu Ala Ala Asp Asn
 1410 1415 1420
 Val Trp Gly Asp Asn Thr Gly Tyr Gln Phe Leu Leu Asp Ala Asp His
 1425 1430 1435 1440
 Asn Thr Phe Gly Ser Val Ile Pro Ala Thr Gly Pro Leu Phe Thr Gly
 1445 1450 1455
 Thr Ala Ser Ser Asn Leu Tyr Ser Ala Asn Phe Glu Tyr Leu Ile Pro
 1460 1465 1470
 Ala Asn Ala Asp Pro Val Val Thr Thr Gln Asn Ile Ile Val Thr Gly
 1475 1480 1485

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Gln Gly Glu Val Val Ile Pro Gly Gly Val Tyr Asp Tyr Cys Ile Thr
 1490 1495 1500
 Asn Pro Glu Pro Ala Ser Gly Lys Met Trp Ile Ala Gly Asp Gly Gly
 1505 1510 1515 1520
 Asn Gln Pro Ala Arg Tyr Asp Asp Phe Thr Phe Glu Ala Gly Lys Lys
 1525 1530 1535
 Tyr Thr Phe Thr Met Arg Arg Ala Gly Met Gly Asp Gly Thr Asp Met
 1540 1545 1550
 Glu Val Glu Asp Asp Ser Pro Ala Ser Tyr Thr Tyr Thr Val Tyr Arg
 1555 1560 1565
 Asp Gly Thr Lys Ile Lys Glu Gly Leu Thr Glu Thr Thr Tyr Arg Asp
 1570 1575 1580
 Ala Gly Met Ser Ala Gln Ser His Glu Tyr Cys Val Glu Val Lys Tyr
 1585 1590 1595 1600
 Ala Ala Gly Val Ser Pro Lys Val Cys Val Asp Tyr Ile Pro Asp Gly
 1605 1610 1615
 Val Ala Asp Val Thr Ala Gln Lys Pro Tyr Thr Leu Thr Val Val Gly
 1620 1625 1630
 Lys Thr Ile Thr Val Thr Cys Gln Gly Glu Ala Met Ile Tyr Asp Met
 1635 1640 1645
 Asn Gly Arg Arg Leu Ala Ala Gly Arg Asn Thr Val Val Tyr Thr Ala
 1650 1655 1660
 Gln Gly Gly Tyr Tyr Ala Val Met Val Val Val Asp Gly Lys Ser Tyr
 1665 1670 1675 1680
 Val Glu Lys Leu Ala Val Lys
 1685

Claims

1 1. A method for the detection of evidence of periodontal disease in human or animal tissue
2 or fluid samples, said method comprising contacting said sample with a DNA probe wherein said
3 probe comprises a detectable single-stranded DNA having a nucleotide sequence sufficiently
4 homologous with the DNA of *Porphyromonas gingivalis* so that the DNA of the probe specifically
5 and selectively hybridizes with the DNA of said bacteria for detection of said probe bound to said
6 homologous DNA.

1 2. The method, according to claim 1, wherein said DNA probe comprises a nucleotide
2 sequence selected from the group consisting of SEQ ID NO. 11, SEQ ID NO. 15, SEQ ID NO. 17,
3 SEQ ID NO. 19, SEQ ID NO. 21, and SEQ ID NO. 23, or a fragment of variant thereof, said
4 fragment or variant having sufficient homology with said sequences to specifically and selectively
5 hybridize thereto.

1 3. The method, according to claim 1, wherein said DNA probe comprises a nucleotide
2 sequence selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ
3 ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 13, SEQ ID NO. 25, and SEQ ID NO. 28, or a fragment or
4 variant thereof.

1 4. The method, according to claim 2, wherein said nucleotide sequence encodes a
2 polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO. 12,
3 SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, and SEQ ID NO. 24, or a
4 fragment or variant thereof.

1 5. A *Porphyromonas gingivalis* gene encoding a polypeptide, said polypeptide having an
2 amino acid sequence selected from the group consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID
3 NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ
4 ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 26, SEQ ID NO. 27, and SEQ ID NO. 29, or a fragment
5 or variant thereof.

1 6. The gene, according to claim 3, said gene comprising the nucleotide sequence selected
2 from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 7, SEQ

3 ID NO. 9, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21,
4 SEQ ID NO. 25, and SEQ ID NO. 28, or a fragment or variant thereof.

1 7. A host cell transformed with a *Porphyromonas gingivalis* gene which encodes a
2 *Porphyromonas gingivalis* antigen, said gene selected from the group consisting of SEQ ID NO.
3 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 13, SEQ ID NO.
4 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 25, and SEQ ID NO. 28, or a
5 fragment or variant thereof.

1 8. The recombinant cell, according to claim 7, which has all of the identifying characteristics
2 of ATCC 67733.

1 9. The recombinant cell, according to claim 7, which has all the identifying characteristics
2 of ATCC 67734.

1 10. A polypeptide wherein said polypeptide has an amino acid sequence selected from the
2 group consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO.
3 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID
4 NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 27, and SEQ ID NO. 29, or a fragment or
5 variant thereof.

1 11. A method for detecting the presence of anti-*Porphyromonas gingivalis* antibodies in
2 a biological fluid sample, said method comprising

- 3 (a) contacting the sample with whole transformed host cell or cell lysate, wherein said
4 cell expresses *Porphyromonas gingivalis*-specific antigens, said contacting done
5 under conditions compatible with specific antigen/antibody immunocomplex
6 formation between said expressed antigens and antibodies present in the sample;
7 and
8 (b) detecting immunocomplex formation by means of a label to thereby detect the
9 presence of *Porphyromonas gingivalis* antibodies in the sample.

1 12. The method, according to claim 11, wherein said *Porphyromonas gingivalis* antigen
2 expressed by the host cell or cell lysate is a polypeptide having the amino acid sequence selected
3 from the group consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ

4 ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20,
5 SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 27, and SEQ ID NO. 29, or a
6 fragment or variant thereof.

1 13. The method, according to claim 11, wherein said *Porphyromonas gingivalis* antigen
2 is encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of
3 SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11,
4 SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO.
5 23, SEQ ID NO. 25, and SEQ ID NO. 28, or a fragment or variant thereof.

1 14. A method for vaccinating a susceptible human or animal host to confer immunity to
2 periodontal disease, said method comprising administering an immunizing amount of a transformed
3 host cell or cell lysate, or a product of a transformed host cell, wherein said cell has been transformed
4 with a DNA fragment which encodes an amino acid sequence selected from the group consisting of
5 SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12,
6 SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO.
7 24, SEQ ID NO. 26, SEQ ID NO. 27, and SEQ ID NO. 29, or a fragment or variant thereof.

1 15. The method, according to claim 14, wherein said DNA fragment has the nucleotide
2 sequence selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ
3 ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ
4 ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, and SEQ ID NO. 28, or a fragment
5 or variant thereof.

1 16. A vaccine for conferring immunity to periodontal disease on a susceptible human or
2 animal host, said vaccine comprising an immunizing amount of a DNA sequence, a host cell
3 transformed with said DNA sequence, or a product or lysate of said transformed host cell, wherein
4 said DNA sequence encodes an amino acid sequence selected from the group consisting of SEQ ID
5 NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 14, SEQ ID
6 NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, and SEQ ID NO. 29,
7 or a fragment or variant thereof.

1 17. The vaccine, according to claim 16, wherein said DNA sequence is sequence selected
2 from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 7, SEQ

3 ID NO. 9, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21,
4 SEQ ID NO. 25, and SEQ ID NO. 28, or a fragment or variant thereof.

1 18. The vaccine, according to claim 16, wherein said transformed host cells are *Salmonella*.

1 19. A monoclonal antibody reagent useful in determining the presence of a periodontal
2 pathogen, said reagent comprising at least one monoclonal antibody species-specific to
3 *Porphyromonas gingivalis*, wherein said monoclonal antibody specifically and selectively binds to
4 a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO. 2,
5 SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14,
6 SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO.
7 26, SEQ ID NO. 27, and SEQ ID NO. 29, or a fragment or variant thereof.

1 20. A kit for detecting evidence of periodontal disease, wherein said kit comprises a
2 *Porphyromonas gingivalis*-specific component selected from the group consisting of the *hagA*,
3 *hagB*, *hagC*, *hagD* gene, or *prtP*, a polypeptide product of said gene, and an antibody to said
4 polypeptide gene product.

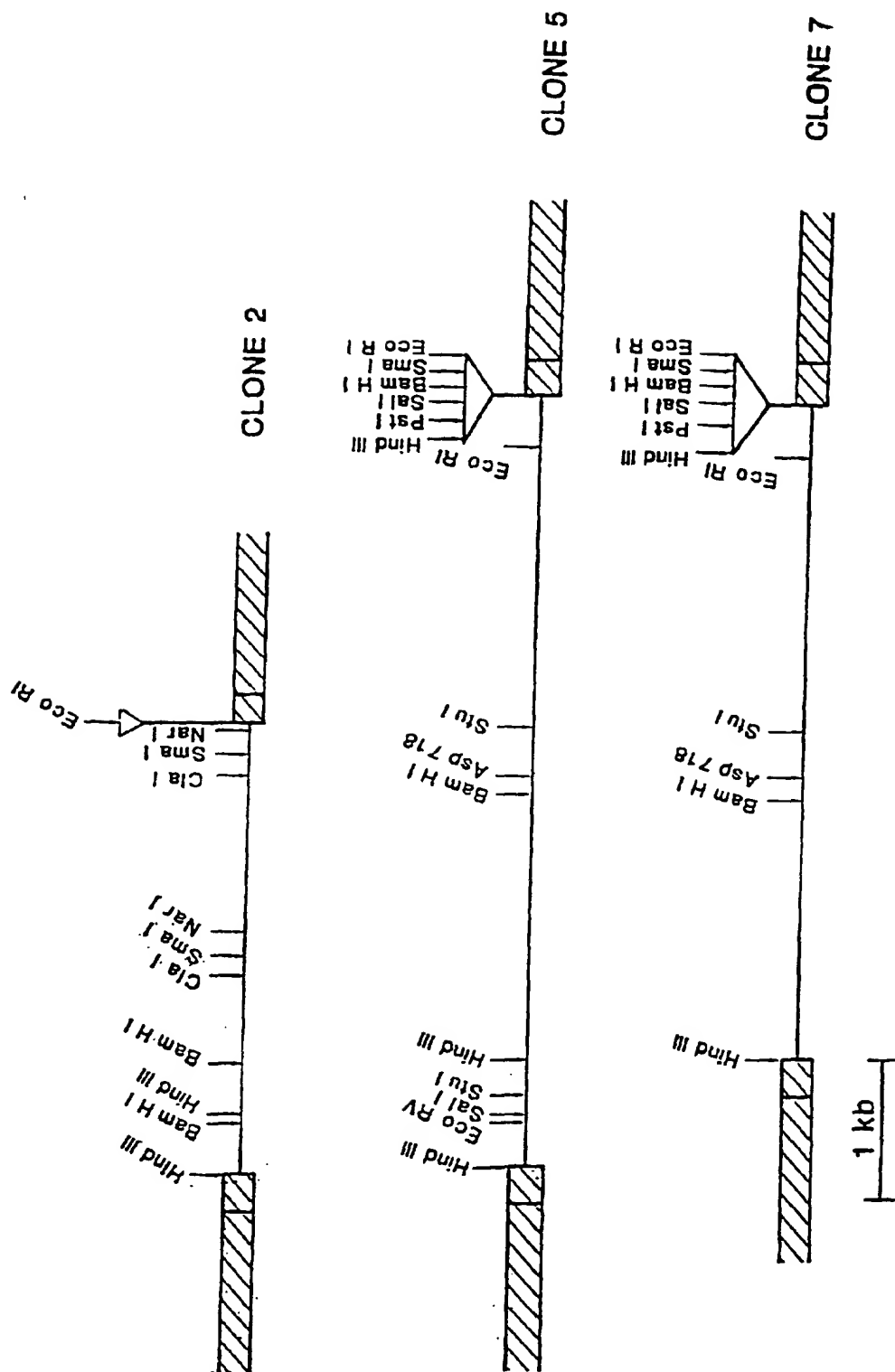
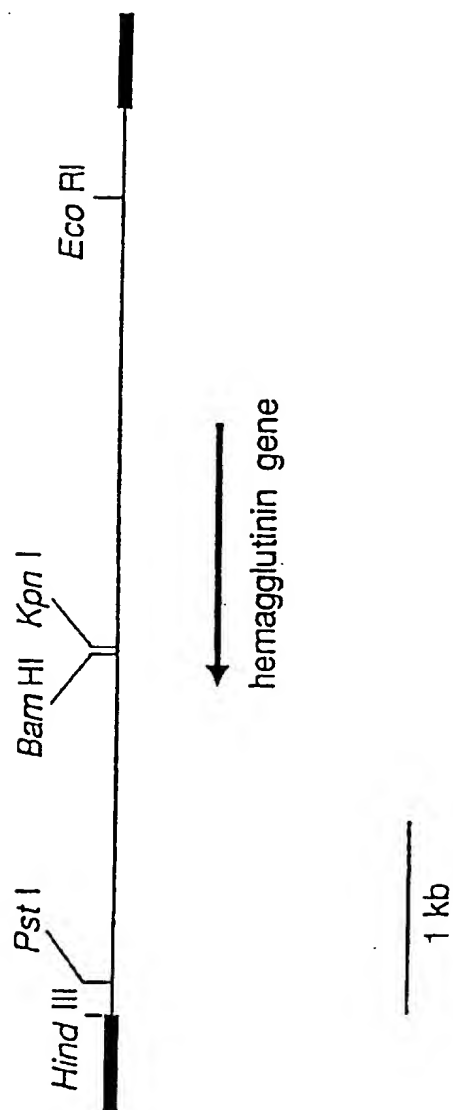


Figure 1

**Figure 2**

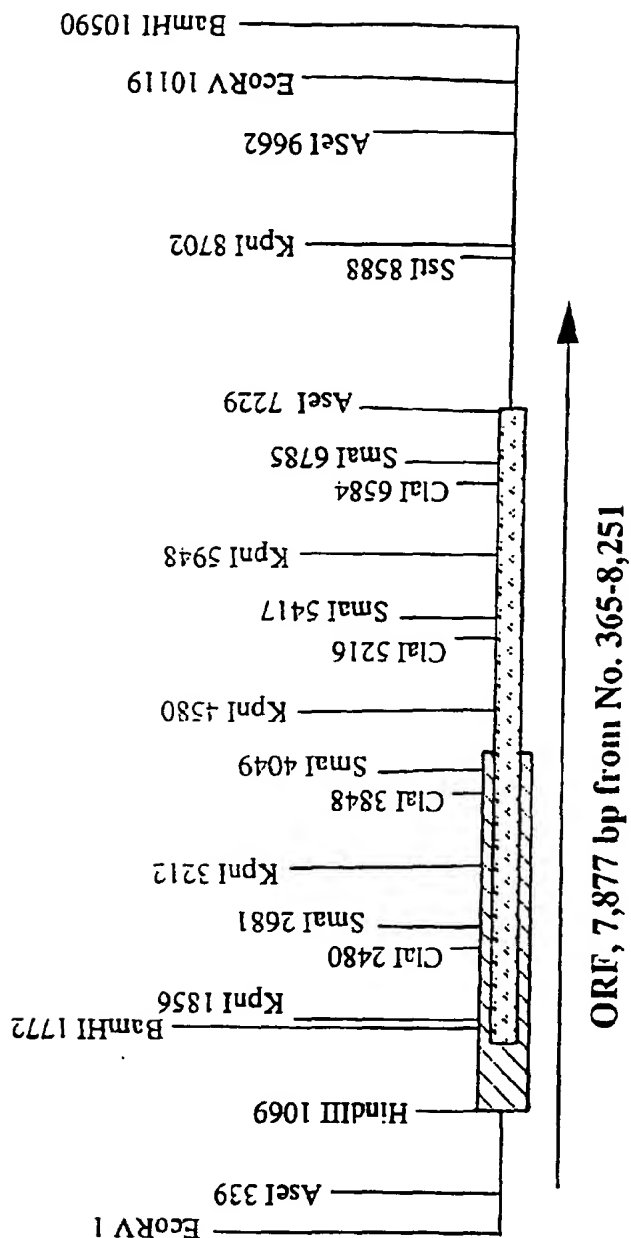
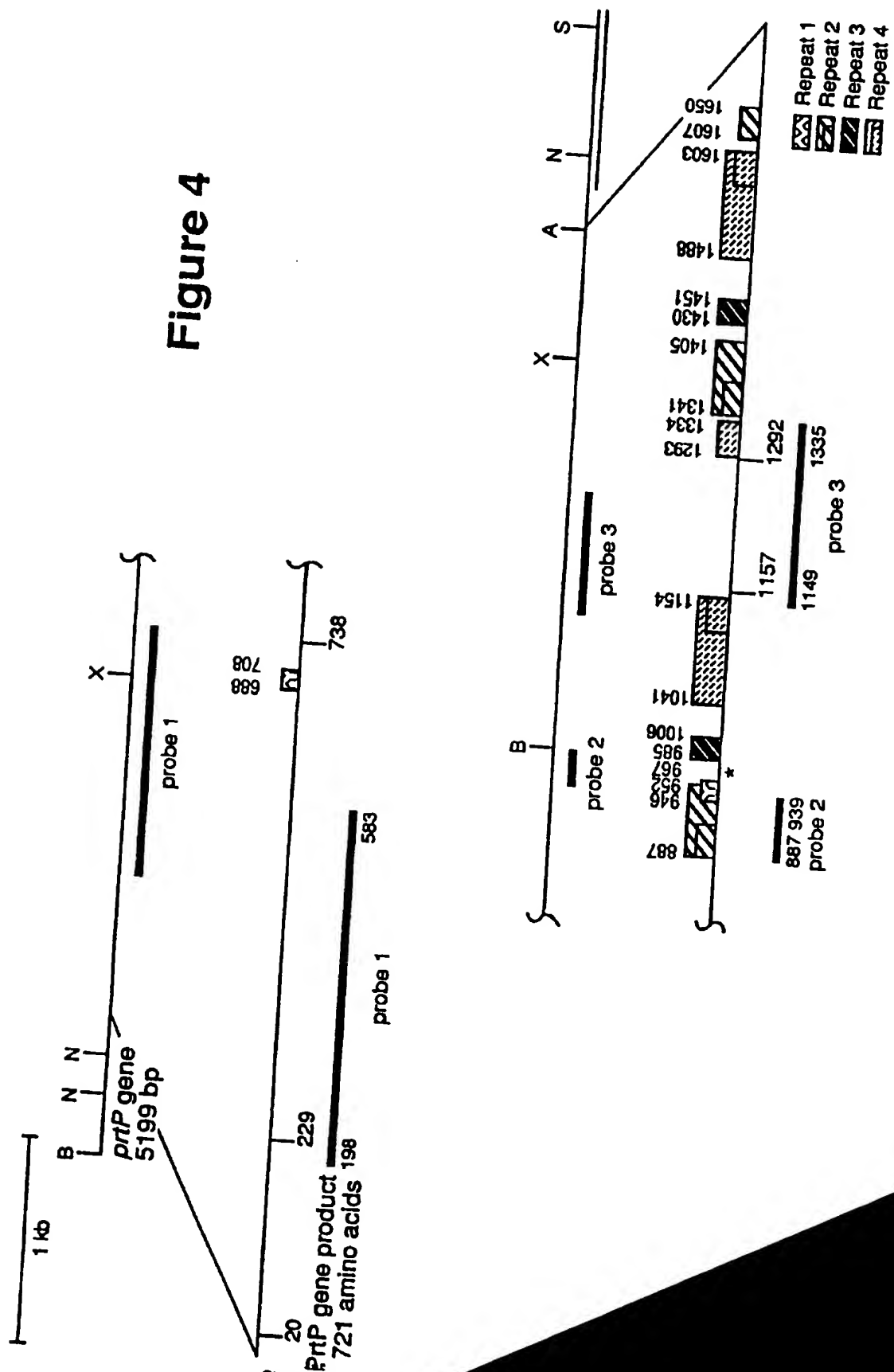


Figure 3

Figure 4



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